

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1	LIB3602-077-Q6-K6-F1	2500354	BLASTX	866	3.00E-93	81	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
2	LIB3602-006-Q1-K1-B6	2500354	BLASTX	862	8.00E-93	81	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
3	LIB3602-076-Q6-K6-F1	2500354	BLASTX	844	1.00E-90	84	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
4	LIB3602-092-Q6-K6-H1	2500354	BLASTX	844	1.00E-90	84	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
5	LIB3602-066-Q1-K6-G9	2500354	BLASTX	840	3.00E-90	82	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
6	LIB3602-074-Q1-K1-B8	2500354	BLASTX	828	8.00E-89	80	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
7	LIB3602-018-Q6-K1-D3	2500354	BLASTX	807	2.00E-86	81	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
8	LIB3602-049-Q6-K1-H3	2500354	BLASTX	769	6.00E-82	81	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
9	LIB3602-093-Q6-K6-G1	2500354	BLASTX	758	1.00E-80	79	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
10	LIB3602-080-Q6-K6-A8	2500354	BLASTX	758	2.00E-80	79	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
11	LIB3602-090-Q6-K6-H7	2500354	BLASTX	757	2.00E-80	79	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
12	LIB3602-028-Q6-K1-D12	2500354	BLASTX	715	1.00E-75	81	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
13	LIB3602-091-Q6-K6-H7	2500354	BLASTX	595	2.00E-75	79	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
14	LIB3602-094-Q6-K6-H7	2500354	BLASTX	583	2.00E-75	78	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
15	LIB3602-058-Q6-K1-G2	2500354	BLASTX	694	3.00E-73	80	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
16	LIB3602-106-Q1-K1-F7	2500354	BLASTX	666	3.00E-73	78	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
17	LIB3602-093-Q6-K6-B12	2500354	BLASTX	666	2.00E-72	78	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
18	LIB3602-046-Q6-K1-H6	2500354	BLASTX	660	3.00E-69	80	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM family protein [Solanum melongena]
19	LIB3602-018-Q6-K1-C3	2500354	BLASTX	620	1.00E-64	73	60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
20	LIB3602-095-Q6-K6-A11	2500354	BLASTX	586	1.00E-64	78	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
21	LIB3602-057-Q6-K1-F8	2500354	BLASTX	609	3.00E-63	78	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
22	LIB3602-076-Q6-K6-A12	2500354	BLASTX	584	3.00E-60	80	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
23	LIB3602-034-Q6-K1-F12	2500354	BLASTX	581	4.00E-60	80	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
24	LIB3602-094-Q6-K6-A11	2500354	BLASTX	572	8.00E-59	76	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
25	LIB3602-032-Q6-K1-A5	2500354	BLASTX	523	3.00E-53	78	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
26	LIB3602-058-Q6-K1-E12	2500354	BLASTX	502	9.00E-51	77	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
27	LIB3602-035-Q1-K1-F12	2500354	BLASTX	494	9.00E-50	77	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
28	LIB3602-038-Q6-K1-B9	2500354	BLASTX	481	2.00E-48	76	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
29	LIB3602-056-Q6-K1-D4	2500354	BLASTX	466	1.00E-46	76	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
30	LIB3602-070-Q1-K1-E9	2500354	BLASTX	462	6.00E-46	72	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
31	LIB3602-023-Q6-K1-H11	2500354	BLASTX	440	1.00E-43	75	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
32	LIB3602-095-Q6-K6-D8	2500354	BLASTX	419	4.00E-41	74	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
33	LIB3602-002-P1-K6-E9	2500354	BLASTX	419	6.00E-41	74	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
34	LIB3602-079-Q6-K6-E1	2500354	BLASTX	390	1.00E-37	66	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
35	LIB3602-055-Q6-K1-A8	2500354	BLASTX	367	5.00E-35	71	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
36	LIB3602-032-Q6-K1-B3	2500354	BLASTX	335	3.00E-31	70	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
37	LIB3602-106-Q1-K1-D7	2500354	BLASTX	186	4.00E-29	66	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
38	LIB3602-018-Q6-K1-B7	2500354	BLASTX	311	1.00E-28	69	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM

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39	LIB3602-093-Q6-K6-E6	2500354	BLASTX	301	2.00E-27	69	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
40	LIB3602-008-Q6-K1-G11	2500354	BLASTX	274	3.00E-24	68	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
41	LIB3602-018-Q6-K1-B1	2500354	BLASTX	202	1.00E-15	50	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L10 (EQM) >gi 1902894 dbj BAA19462.1 (AB001891) QM
42	LIB3602-028-Q6-K1-H6	2851508	BLASTX	541	3.00E-55	62	family protein [Solanum melongena] 60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
43	LIB3602-101-Q1-K1-B12	2851508	BLASTX	541	3.00E-55	62	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
44	LIB3602-062-Q6-K1-G12	2851508	BLASTX	541	3.00E-55	62	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
45	LIB3602-009-Q6-K1-D1	2851508	BLASTX	541	3.00E-55	62	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
46	LIB3602-078-Q6-K6-G1	2851508	BLASTX	541	4.00E-55	62	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
47	LIB3602-073-Q1-K1-E10	2851508	BLASTX	536	1.00E-54	61	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
48	LIB3602-067-Q1-K1-G5	2851508	BLASTX	536	1.00E-54	61	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana]

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
57	LIB3602-070-Q1-K1-F1	2851508	BLASTX	490	3.00E-49	60	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
58	LIB3602-056-Q6-K1-B2	2851508	BLASTX	485	9.00E-49	65	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
59	LIB3602-040-Q6-K1-G5	2851508	BLASTX	468	9.00E-47	60	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
60	LIB3602-116-Q1-K1-G12	2851508	BLASTX	468	1.00E-46	60	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
61	LIB3602-108-Q1-K1-B3	2851508	BLASTX	364	7.00E-45	65	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
62	LIB3602-051-Q6-K1-E3	2851508	BLASTX	443	9.00E-44	58	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
63	LIB3602-020-Q6-K1-A2	2851508	BLASTX	435	5.00E-43	64	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
64	LIB3602-095-Q6-K6-G12	2851508	BLASTX	429	4.00E-42	58	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
65	LIB3602-044-Q6-K1-C10	2851508	BLASTX	418	4.00E-41	67	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar

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							to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
66	LIB3602-004-Q1-K1-G2	2851508	BLASTX	419	5.00E-41	60	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
67	LIB3602-082-Q6-K6-G1	2851508	BLASTX	416	1.00E-40	59	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
68	LIB3602-109-Q1-K1-D10	2851508	BLASTX	411	4.00E-40	60	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
69	LIB3602-049-Q6-K1-D8	2851508	BLASTX	394	2.00E-38	71	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
70	LIB3602-015-Q6-K1-E7	2851508	BLASTX	391	9.00E-38	59	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
71	LIB3602-093-Q6-K6-C9	2851508	BLASTX	374	1.00E-35	52	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
72	LIB3602-021-Q6-K1-H6	2851508	BLASTX	347	5.00E-33	71	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
73	LIB3602-102-Q1-K1-C1	2851508	BLASTX	327	3.00E-30	56	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene.

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							[Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
74	LIB3602-102-Q1-K1-D2	2851508	BLASTX	261	1.00E-22	55	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
75	LIB3602-059-Q6-K1-A8	2851508	BLASTX	255	7.00E-22	54	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
76	LIB3602-040-Q6-K1-G9	2851508	BLASTX	246	6.00E-21	53	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
77	LIB3602-109-Q1-K1-H11	2851508	BLASTX	215	1.00E-17	57	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
78	LIB3602-009-Q6-K1-D2	2851508	BLASTX	200	1.00E-15	62	60S RIBOSOMAL PROTEIN L21 >gi 2160162 gb AAB60725.1 (AC000132) Similar to ribosomal protein L21 (gb L38826). ESTs gb AA395597,gb ATTS5197 come from this gene. [Arabidopsis thaliana] >gi 3482935 gb AAC33220.1 (AC003970) Putative ribosomal protein L21 [Ar
79	LIB3602-080-Q6-K6-H6	4139216	BLASTX	800	1.00E-85	79	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
80	LIB3602-088-Q6-K6-C6	4139216	BLASTX	732	1.00E-77	75	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
81	LIB3602-090-Q6-K6-H2	4139216	BLASTX	713	2.00E-75	75	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
82	LIB3602-071-Q1-K1-C6	4139216	BLASTX	707	1.00E-74	74	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
83	LIB3602-027-Q6-K1-E8	4139216	BLASTX	694	3.00E-73	74	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
84	LIB3602-074-Q1-K1-F10	4139216	BLASTX	689	2.00E-72	75	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
85	LIB3602-028-Q6-K1-F7	4139216	BLASTX	688	2.00E-72	75	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
86	LIB3602-106-Q1-K1-E11	4139216	BLASTX	686	3.00E-72	74	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
87	LIB3602-113-Q1-K1-A8	4139216	BLASTX	668	5.00E-70	72	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
88	LIB3602-063-Q1-K6-B5	4139216	BLASTX	656	1.00E-68	74	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
89	LIB3602-092-Q6-K6-A8	4139216	BLASTX	643	4.00E-67	72	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
90	LIB3602-118-Q1-K1-H5	4139216	BLASTX	479	4.00E-65	77	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
91	LIB3602-103-Q1-K1-E7	4139216	BLASTX	611	2.00E-63	77	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
92	LIB3602-046-Q6-K1-B10	4139216	BLASTX	605	8.00E-63	78	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
93	LIB3602-040-Q6-K1-H5	4139216	BLASTX	603	2.00E-62	78	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
94	LIB3602-015-Q6-K1-D11	4139216	BLASTX	583	4.00E-60	80	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
95	LIB3602-035-Q1-K1-D5	4139216	BLASTX	580	8.00E-60	80	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
96	LIB3602-063-Q1-K6-F12	4139216	BLASTX	569	2.00E-58	68	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
97	LIB3602-088-Q6-K6-A2	4139216	BLASTX	561	1.00E-57	64	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
98	LIB3602-111-Q1-K1-D10	4139216	BLASTX	437	4.00E-57	68	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
99	LIB3602-094-Q6-K6-D5	4139216	BLASTX	544	2.00E-55	71	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
100	LIB3602-011-Q6-K1-H9	4139216	BLASTX	538	7.00E-55	71	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
101	LIB3602-073-Q1-K1-B7	4139216	BLASTX	538	8.00E-55	71	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
102	LIB3602-037-Q6-K1-G7	4139216	BLASTX	530	4.00E-54	74	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
103	LIB3602-113-Q1-K1-E12	4139216	BLASTX	531	5.00E-54	71	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
104	LIB3602-071-Q1-K1-B11	4139216	BLASTX	517	2.00E-52	74	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
105	LIB3602-026-Q6-K1-E12	4139216	BLASTX	503	9.00E-51	71	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
106	LIB3602-085-Q6-K1-F8	4139216	BLASTX	499	3.00E-50	71	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
107	LIB3602-034-Q6-K1-D5	4139216	BLASTX	469	4.00E-47	85	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
108	LIB3602-120-Q1-K1-E1	4139216	BLASTX	450	2.00E-44	70	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
109	LIB3602-108-Q1-K1-D3	4139216	BLASTX	446	3.00E-44	62	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
110	LIB3602-117-Q1-K1-D10	4139216	BLASTX	215	1.00E-21	73	(AF104630) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
111	LIB3602-043-Q6-K1-G6	548774	BLASTX	665	1.00E-69	59	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
112	LIB3602-074-Q1-K1-G11	548774	BLASTX	634	5.00E-66	59	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
113	LIB3602-041-Q6-K1-D5	548774	BLASTX	631	9.00E-66	62	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
114	LIB3602-086-Q6-K1-E6	548774	BLASTX	598	7.00E-62	64	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a,

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
115	LIB3602-012-Q6-K1-A6	548774	BLASTX	596	1.00E-61	60	cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa] 60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
116	LIB3602-039-Q6-K1-G5	548774	BLASTX	592	3.00E-61	65	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
117	LIB3602-107-Q1-K1-B7	548774	BLASTX	570	1.00E-58	59	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
118	LIB3602-047-Q6-K1-C12	548774	BLASTX	568	2.00E-58	65	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
119	LIB3602-094-Q6-K6-H9	548774	BLASTX	546	9.00E-56	56	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
120	LIB3602-091-Q6-K6-H9	548774	BLASTX	539	6.00E-55	55	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
121	LIB3602-108-Q1-K1-C12	548774	BLASTX	530	6.00E-54	58	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
122	LIB3602-077-Q6-K6-H6	548774	BLASTX	526	2.00E-53	55	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
123	LIB3602-116-Q1-K1-H9	548774	BLASTX	414	2.00E-53	62	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
124	LIB3602-043-Q6-K1-G4	548774	BLASTX	524	3.00E-53	59	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
125	LIB3602-052-Q6-K1-F5	548774	BLASTX	494	8.00E-50	64	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
126	LIB3602-001-P1-K6-G6	548774	BLASTX	471	5.00E-47	59	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
127	LIB3602-007-Q1-K1-C12	548774	BLASTX	459	2.00E-45	52	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
128	LIB3602-006-Q1-K1-H5	548774	BLASTX	444	8.00E-44	52	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
129	LIB3602-059-Q6-K1-F12	548774	BLASTX	427	7.00E-42	56	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
130	LIB3602-103-Q1-K1-C12	548774	BLASTX	383	2.00E-41	59	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
131	LIB3602-029-Q6-K1-F9	548774	BLASTX	414	2.00E-40	62	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
132	LIB3602-019-Q6-K1-B5	548774	BLASTX	389	1.00E-37	72	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
133	LIB3602-056-Q6-K1-B8	548774	BLASTX	386	3.00E-37	58	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
134	LIB3602-080-Q6-K6-B9	548774	BLASTX	298	4.00E-36	60	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
135	LIB3602-048-Q6-K1QA-B9	548774	BLASTX	374	8.00E-36	62	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
136	LIB3602-053-Q6-K1-H1	548774	BLASTX	366	8.00E-35	63	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
137	LIB3602-076-Q6-K6-H10	548774	BLASTX	357	1.00E-33	62	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
138	LIB3602-063-Q1-K6-F1	548774	BLASTX	348	8.00E-33	54	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
139	LIB3602-032-Q6-K1-E6	548774	BLASTX	315	6.00E-29	76	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
140	LIB3602-077-Q6-K6-C12	548774	BLASTX	304	2.00E-27	62	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
141	LIB3602-081-Q6-K6-E9	548774	BLASTX	166	2.00E-11	57	60S RIBOSOMAL PROTEIN L7A >gi 542158 pir S38360 ribosomal protein L7a, cytosolic - rice >gi 303855 dbj BAA02156.1 (D12631) ribosomal protein L7A [Oryza sativa]
142	LIB3602-094-Q6-K6-B5	6440817	BLASTX	391	1.00E-37	62	(AU066512) hypothetical protein [Chlamydomonas sp.]
143	LIB3602-054-Q6-K1-E10	6440817	BLASTX	383	8.00E-37	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
144	LIB3602-045-Q6-K1-E3	6440817	BLASTX	383	9.00E-37	61	(AU066512) hypothetical protein [Chlamydomonas sp.]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
145	LIB3602-103-Q1-K1-B9	6440817	BLASTX	383	9.00E-37	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
146	LIB3602-070-Q1-K1-D3	6440817	BLASTX	383	1.00E-36	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
147	LIB3602-094-Q6-K6-G5	6440817	BLASTX	383	1.00E-36	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
148	LIB3602-087-Q6-K1-G6	6440817	BLASTX	383	1.00E-36	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
149	LIB3602-104-Q1-K1-E12	6440817	BLASTX	383	1.00E-36	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
150	LIB3602-029-Q6-K1-F4	6440817	BLASTX	383	1.00E-36	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
151	LIB3602-065-Q1-K6-E9	6440817	BLASTX	383	1.00E-36	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
152	LIB3602-084-Q6-K1-E1	6440817	BLASTX	379	3.00E-36	60	(AU066512) hypothetical protein [Chlamydomonas sp.]
153	LIB3602-066-Q1-K6-A4	6440817	BLASTX	379	4.00E-36	62	(AU066512) hypothetical protein [Chlamydomonas sp.]
154	LIB3602-107-Q1-K1-C11	6440817	BLASTX	378	4.00E-36	64	(AU066512) hypothetical protein [Chlamydomonas sp.]
155	LIB3602-060-Q6-K1-H8	6440817	BLASTX	377	5.00E-36	61	(AU066512) hypothetical protein [Chlamydomonas sp.]
156	LIB3602-060-Q6-K1-F2	6440817	BLASTX	370	3.00E-35	60	(AU066512) hypothetical protein [Chlamydomonas sp.]
157	LIB3602-058-Q6-K1-H10	6440817	BLASTX	365	1.00E-34	62	(AU066512) hypothetical protein [Chlamydomonas sp.]
158	LIB3602-005-Q1-K1-E11	6440817	BLASTX	360	6.00E-34	63	(AU066512) hypothetical protein [Chlamydomonas sp.]
159	LIB3602-048-Q6-K1QA-G5	6440817	BLASTX	354	2.00E-33	64	(AU066512) hypothetical protein [Chlamydomonas sp.]
160	LIB3602-037-Q6-K1-H2	6440817	BLASTX	350	6.00E-33	73	(AU066512) hypothetical protein [Chlamydomonas sp.]
161	LIB3602-111-Q1-K1-E3	6440817	BLASTX	339	6.00E-33	63	(AU066512) hypothetical protein [Chlamydomonas sp.]
162	LIB3602-085-Q6-K1-E8	6440817	BLASTX	289	2.00E-29	66	(AU066512) hypothetical protein [Chlamydomonas sp.]
163	LIB3602-079-Q6-K6-H11	6440817	BLASTX	290	8.00E-26	70	(AU066512) hypothetical protein [Chlamydomonas sp.]
164	LIB3602-059-Q6-K1-B9	6440817	BLASTX	285	1.00E-25	72	(AU066512) hypothetical protein [Chlamydomonas sp.]
165	LIB3602-071-Q1-K1-E7	6440817	BLASTX	277	2.00E-24	69	(AU066512) hypothetical protein [Chlamydomonas sp.]
166	LIB3602-116-Q1-K1-B5	6440817	BLASTX	271	2.00E-23	78	(AU066512) hypothetical protein [Chlamydomonas sp.]
167	LIB3602-012-Q6-K1-D10	6440817	BLASTX	263	1.00E-22	69	(AU066512) hypothetical protein [Chlamydomonas sp.]
168	LIB3602-045-Q6-K1-E4	6440817	BLASTX	196	6.00E-15	44	(AU066512) hypothetical protein [Chlamydomonas sp.]
169	LIB3602-049-Q6-K1-F3	6440817	BLASTX	184	2.00E-13	65	(AU066512) hypothetical protein [Chlamydomonas sp.]
170	LIB3602-029-Q6-K1-F5	6440817	BLASTX	155	5.00E-10	75	(AU066512) hypothetical protein [Chlamydomonas sp.]
171	LIB3602-022-Q6-K1-C12	485518	BLASTX	620	1.00E-64	96	ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
172	LIB3602-054-Q6-K1-C6	485518	BLASTX	620	1.00E-64	96	ubiquitin/ribosomal polypeptide [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629) ubiquitin/ribosomal polypeptide [Oryza sativa]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
173	LIB3602-079-Q6-K6-F2	485518	BLASTX	620	2.00E-64	96	ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
174	LIB3602-034-Q6-K1-F6	485518	BLASTX	620	2.00E-64	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
175	LIB3602-038-Q6-K1-H6	485518	BLASTX	620	2.00E-64	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
176	LIB3602-042-Q6-K1-D8	485518	BLASTX	620	2.00E-64	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
177	LIB3602-077-Q6-K6-C3	485518	BLASTX	620	2.00E-64	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
178	LIB3602-029-Q6-K1-G1	485518	BLASTX	620	2.00E-64	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
179	LIB3602-111-Q1-K1-G1	485518	BLASTX	614	9.00E-64	95	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
180	LIB3602-112-Q1-K1-E1	485518	BLASTX	611	2.00E-63	95	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
181	LIB3602-056-Q6-K1-G9	485518	BLASTX	594	1.00E-61	90	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
182	LIB3602-035-Q1-K1-F6	485518	BLASTX	588	1.00E-60	94	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
183	LIB3602-023-Q6-K1-B9	485518	BLASTX	582	5.00E-60	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
184	LIB3602-091-Q6-K6-B8	485518	BLASTX	577	2.00E-59	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
185	LIB3602-041-Q6-K1-D4	485518	BLASTX	577	2.00E-59	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
186	LIB3602-085-Q6-K1-F1	485518	BLASTX	572	8.00E-59	95	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
187	LIB3602-005-Q1-K1-C4	485518	BLASTX	560	2.00E-57	93	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
188	LIB3602-108-Q1-K1-B6	485518	BLASTX	411	2.00E-57	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
189	LIB3602-047-Q6-K1-D10	485518	BLASTX	553	1.00E-56	95	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
190	LIB3602-101-Q1-K1-D1	485518	BLASTX	420	2.00E-56	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
191	LIB3602-009-Q6-K1-B12	485518	BLASTX	511	9.00E-52	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
192	LIB3602-094-Q6-K6-D11	485518	BLASTX	504	7.00E-51	95	ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
193	LIB3602-113-Q1-K1-A5	485518	BLASTX	482	2.00E-48	94	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
194	LIB3602-112-Q1-K1-A5	485518	BLASTX	482	3.00E-48	94	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
195	LIB3602-108-Q1-K1-D2	485518	BLASTX	298	3.00E-47	93	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
196	LIB3602-032-Q6-K1-F10	485518	BLASTX	470	5.00E-47	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
197	LIB3602-025-Q6-K1-G12	485518	BLASTX	456	2.00E-45	89	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
198	LIB3602-038-Q6-K1-F12	485518	BLASTX	423	8.00E-42	92	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
199	LIB3602-014-Q6-K1-G3	485518	BLASTX	386	3.00E-37	96	ubiquitin/ribosomal polyprotein [Oryza sativa] ubiquitin / ribosomal protein CEP52 - rice >gi 303857 dbj BAA02154.1 (D12629)
200	LIB3602-079-Q6-K6-B12	7440926	BLASTX	715	1.00E-75	73	ubiquitin/ribosomal polyprotein [Oryza sativa] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
201	LIB3602-065-Q1-K6-E3	7440926	BLASTX	712	3.00E-75	72	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
202	LIB3602-002-P1-K6-B1	7440926	BLASTX	712	3.00E-75	72	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
203	LIB3602-023-Q6-K1-F5	7440926	BLASTX	690	1.00E-72	74	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
204	LIB3602-105-Q1-K1-B12	7440926	BLASTX	669	3.00E-70	68	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
205	LIB3602-028-Q6-K1-B11	7440926	BLASTX	646	1.00E-67	74	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
206	LIB3602-045-Q6-K1-A3	7440926	BLASTX	625	4.00E-65	76	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
207	LIB3602-045-Q6-K1-B11	7440926	BLASTX	611	2.00E-63	77	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
208	LIB3602-056-Q6-K1-D10	7440926	BLASTX	603	1.00E-62	75	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
209	LIB3602-091-Q6-K6-H8	7440926	BLASTX	410	2.00E-61	69	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
210	LIB3602-094-Q6-K6-H8	7440926	BLASTX	420	5.00E-61	71	60S ribosomal protein L18A [Arabidopsis thaliana] ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
211	LIB3602-032-Q6-K1-A3	7440926	BLASTX	588	7.00E-61	79	ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
212	LIB3602-115-Q1-K1-H9	7440926	BLASTX	420	1.00E-60	71	60S ribosomal protein L18A [Arabidopsis thaliana] >gi 3128228 gb AAC26708.1 (AC004077)
213	LIB3602-019-Q6-K1-B10	7440926	BLASTX	566	3.00E-58	74	ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
214	LIB3602-101-Q1-K1-B10	7440926	BLASTX	547	4.00E-56	74	60S ribosomal protein L18A [Arabidopsis thaliana] >gi 3128228 gb AAC26708.1 (AC004077)
215	LIB3602-072-Q1-K1-D6	7440926	BLASTX	420	5.00E-55	71	ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
216	LIB3602-037-Q6-K1-G3	7440926	BLASTX	503	1.00E-54	79	60S ribosomal protein L18A [Arabidopsis thaliana] >gi 3128228 gb AAC26708.1 (AC004077)
217	LIB3602-068-Q1-K1-C4	7440926	BLASTX	364	6.00E-52	65	ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
218	LIB3602-028-Q6-K1-A7	7440926	BLASTX	492	1.00E-49	72	60S ribosomal protein L18A [Arabidopsis thaliana] >gi 3128228 gb AAC26708.1 (AC004077)
219	LIB3602-046-Q6-K1-G4	7440926	BLASTX	489	3.00E-49	71	ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
220	LIB3602-023-Q6-K1-F3	7440926	BLASTX	395	4.00E-38	71	60S ribosomal protein L18A [Arabidopsis thaliana] >gi 3128228 gb AAC26708.1 (AC004077)
221	LIB3602-015-Q6-K1-D2	7440926	BLASTX	333	7.00E-31	69	ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
222	LIB3602-028-Q6-K1-H3	7440926	BLASTX	333	7.00E-31	69	60S ribosomal protein L18A [Arabidopsis thaliana] >gi 3128228 gb AAC26708.1 (AC004077)
223	LIB3602-021-Q6-K1-A12	7440926	BLASTX	320	8.00E-30	73	ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
224	LIB3602-028-Q6-K1-B5	7440926	BLASTX	253	3.00E-22	83	60S ribosomal protein L18A [Arabidopsis thaliana] >gi 3128228 gb AAC26708.1 (AC004077)
225	LIB3602-003-Q1-K1-H9	7440926	BLASTX	254	9.00E-22	64	ribosomal protein L18a, cytosolic - Arabidopsis thaliana >gi 3128228 gb AAC26708.1 (AC004077)
226	LIB3602-089-Q6-K6-A11	7440926	BLASTX	171	5.00E-12	56	60S ribosomal protein L18A [Arabidopsis thaliana] >gi 3128228 gb AAC26708.1 (AC004077)
227	LIB3602-094-Q6-K6-B6	266945	BLASTX	606	8.00E-63	64	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
228	LIB3602-095-Q6-K6-B6	266945	BLASTX	601	3.00E-62	64	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
229	LIB3602-089-Q6-K6-B6	266945	BLASTX	595	2.00E-61	64	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
230	LIB3602-018-Q6-K1-C6	266945	BLASTX	587	1.00E-60	63	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
231	LIB3602-015-Q6-K1-D1	266945	BLASTX	586	2.00E-60	65	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
232	LIB3602-073-Q1-K1-F6	266945	BLASTX	584	3.00E-60	64	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
233	LIB3602-113-Q1-K1-F7	266945	BLASTX	583	4.00E-60	64	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
234	LIB3602-018-Q6-K1-C5	266945	BLASTX	581	6.00E-60	63	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
235	LIB3602-073-Q1-K1-C6	266945	BLASTX	579	1.00E-59	64	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
236	LIB3602-091-Q6-K6-G2	266945	BLASTX	567	3.00E-58	64	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
237	LIB3602-004-Q1-K1-B9	266945	BLASTX	566	5.00E-58	65	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
238	LIB3602-069-Q1-K1-B6	266945	BLASTX	533	3.00E-54	66	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
239	LIB3602-015-Q6-K1-D8	266945	BLASTX	528	1.00E-53	66	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
240	LIB3602-076-Q6-K6-E6	266945	BLASTX	521	8.00E-53	66	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9,

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
241	LIB3602-011-Q6-K1-B8	266945	BLASTX	518	2.00E-52	62	cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum] 60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
242	LIB3602-102-Q1-K1-A8	266945	BLASTX	515	3.00E-52	66	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
243	LIB3602-070-Q1-K1-B6	266945	BLASTX	513	7.00E-52	66	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
244	LIB3602-045-Q6-K1-A6	266945	BLASTX	505	4.00E-51	65	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
245	LIB3602-041-Q6-K1-H1	266945	BLASTX	494	9.00E-50	67	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
246	LIB3602-045-Q6-K1-G6	266945	BLASTX	487	6.00E-49	63	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
247	LIB3602-013-Q6-K1-F2	266945	BLASTX	486	7.00E-49	63	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
248	LIB3602-012-Q6-K1-C2	266945	BLASTX	463	5.00E-46	62	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
249	LIB3602-092-Q6-K6-D9	266945	BLASTX	203	4.00E-29	57	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
250	LIB3602-015-Q6-K1-D9	266945	BLASTX	214	2.00E-21	42	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]
251	LIB3602-115-Q1-K1-E1	266945	BLASTX	192	9.00E-15	74	60S RIBOSOMAL PROTEIN L9 (GIBBERELLIN-REGULATED PROTEIN GA) >gi 100065 pir S19978 ribosomal protein L9, cytosolic - garden pea >gi 20727 emb CAA46273.1 (X65155) GA [Pisum sativum]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
252	LIB3602-100-Q1-K1-B9	115826	BLASTX	489	4.00E-49	77	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
253	LIB3602-107-Q1-K1-D5	115826	BLASTX	464	4.00E-46	77	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
254	LIB3602-044-Q6-K1-B10	115826	BLASTX	463	4.00E-46	77	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
255	LIB3602-115-Q1-K1-D6	115826	BLASTX	414	4.00E-41	80	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
256	LIB3602-070-Q1-K1-G8	115826	BLASTX	414	1.00E-40	80	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
257	LIB3602-102-Q1-K1-A2	115826	BLASTX	302	2.00E-40	82	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
258	LIB3602-118-Q1-K1-D5	115826	BLASTX	211	3.00E-34	86	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
259	LIB3602-044-Q6-K1-F3	115826	BLASTX	344	3.00E-32	76	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
260	LIB3602-052-Q6-K1-D11	115826	BLASTX	331	9.00E-31	77	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii >gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii]
261	LIB3602-083-Q6-K6-E3	115826	BLASTX	330	1.00E-30	61	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
262	LIB3602-118-Q1-K1-F7	115826	BLASTX	329	2.00E-30	79	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
263	LIB3602-037-Q6-K1-C3	115826	BLASTX	329	2.00E-30	79	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
264	LIB3602-022-Q6-K1-H7	115826	BLASTX	319	2.00E-29	76	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
265	LIB3602-112-Q1-K1-A10	115826	BLASTX	319	2.00E-29	76	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
266	LIB3602-089-Q6-K6-A10	115826	BLASTX	315	6.00E-29	75	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
267	LIB3602-017-Q6-K1-A10	115826	BLASTX	293	2.00E-26	75	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
268	LIB3602-004-Q1-K1-B10	115826	BLASTX	278	1.00E-24	57	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
269	LIB3602-027-Q6-K1-G9	115826	BLASTX	266	3.00E-23	78	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
270	LIB3602-106-Q1-K1-B9	115826	BLASTX	225	2.00E-20	49	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99371 pir S14518 chlorophyll a/b-binding protein - Chlamydomonas moewusii
271	LIB3602-044-Q6-K1-G12	115826	BLASTX	224	2.00E-18	76	>gi 18063 emb CAA38635.1 (X54856) chlorophyll a/b-binding protein [Chlamydomonas moewusii] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
281	LIB3602-049-Q6-K1-D5	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
282	LIB3602-042-Q6-K1-B2	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
283	LIB3602-061-Q6-K1-H5	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
284	LIB3602-077-Q6-K6-F9	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
285	LIB3602-079-Q6-K6-A3	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
286	LIB3602-047-Q6-K1-A2	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
287	LIB3602-017-Q6-K1-F8	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
288	LIB3602-017-Q6-K1-C12	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
289	LIB3602-018-Q6-K1-E12	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
290	LIB3602-012-Q6-K1-E12	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
291	LIB3602-026-Q6-K1-A12	7440560	BLASTX	247	6.00E-21	71	(AL161594) ribosomal protein S25 [Arabidopsis thaliana] ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
292	LIB3602-026-Q6-K1-A5	7440560	BLASTX	247	6.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
293	LIB3602-015-Q6-K1-C12	7440560	BLASTX	247	7.00E-21	71	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
294	LIB3602-109-Q1-K1-H2	7440560	BLASTX	239	5.00E-20	69	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
295	LIB3602-109-Q1-K1-C2	7440560	BLASTX	238	6.00E-20	69	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
296	LIB3602-101-Q1-K1-A1	7440560	BLASTX	237	9.00E-20	68	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
297	LIB3602-087-Q6-K1-H9	7440560	BLASTX	229	1.00E-18	70	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
298	LIB3602-021-Q6-K1-D5	7440560	BLASTX	215	2.00E-17	76	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
299	LIB3602-106-Q1-K1-D12	7440560	BLASTX	212	1.00E-16	74	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1 (AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1 (AL161594) ribosomal protein S25 [Arabidopsis thaliana]
300	LIB3602-058-Q6-K1-C7	7440560	BLASTX	160	3.00E-11	67	ribosomal protein S25, cytosolic - Arabidopsis thaliana >gi 4914432 emb CAB43635.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							(AL050351) ribosomal protein S25 [Arabidopsis thaliana] >gi 7270903 emb CAB80583.1
							(AL161594) ribosomal protein S25 [Arabidopsis thaliana]
301	LIB3602-017-Q6-K1-E11	6094037	BLASTX	595	1.00E-61	81	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
302	LIB3602-067-Q1-K1-H1	6094037	BLASTX	595	2.00E-61	81	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
303	LIB3602-074-Q1-K1-H1	6094037	BLASTX	595	2.00E-61	81	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
304	LIB3602-041-Q6-K1-G12	6094037	BLASTX	591	5.00E-61	81	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
305	LIB3602-007-Q1-K1-B11	6094037	BLASTX	573	5.00E-59	84	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
306	LIB3602-069-Q1-K1-H8	6094037	BLASTX	564	7.00E-58	85	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
307	LIB3602-050-Q6-K1-A1	6094037	BLASTX	560	1.00E-57	84	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
308	LIB3602-009-Q6-K1-H7	6094037	BLASTX	536	8.00E-55	82	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
309	LIB3602-053-Q6-K1-G11	6094037	BLASTX	526	1.00E-53	73	>gi 2706454 emb CAA15912.1 (AL021046) 60s riboso 60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
310	LIB3602-014-Q6-K1-F6	6094037	BLASTX	513	4.00E-52	80	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
311	LIB3602-009-Q6-K1-H8	6094037	BLASTX	487	5.00E-49	85	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
312	LIB3602-023-Q6-K1-H4	6094037	BLASTX	487	6.00E-49	85	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
313	LIB3602-042-Q6-K1-D1	6094037	BLASTX	473	2.00E-47	84	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
314	LIB3602-101-Q1-K1-A6	6094037	BLASTX	391	1.00E-46	87	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
315	LIB3602-002-P1-K6-B12	6094037	BLASTX	450	1.00E-44	73	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
316	LIB3602-039-Q6-K1-C12	6094037	BLASTX	437	3.00E-43	85	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
317	LIB3602-028-Q6-K1-D5	6094037	BLASTX	437	3.00E-43	85	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
318	LIB3602-018-Q6-K1-B9	6094037	BLASTX	386	2.00E-37	86	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
319	LIB3602-060-Q6-K1-C8	6094037	BLASTX	369	3.00E-35	79	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
320	LIB3602-004-Q1-K1-D2	6094037	BLASTX	345	2.00E-32	80	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
321	LIB3602-071-Q1-K1-A3	6094037	BLASTX	342	7.00E-32	84	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
322	LIB3602-106-Q1-K1-G9	6094037	BLASTX	291	4.00E-26	72	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
323	LIB3602-001-P1-K6-H2	6094037	BLASTX	261	7.00E-23	84	60S RIBOSOMAL PROTEIN L23 >gi 7440854 pir T11639 ribosomal protein L17 - fission yeast (Schizosaccharomyces pombe) >gi 7490001 pir T40942 60s ribosomal protein - fission yeast (Schizosaccharomyces pombe) >gi 2706454 emb CAA15912.1 (AL021046) 60s riboso
324	LIB3602-081-Q6-K6-E6	730557	BLASTX	388	2.00E-37	62	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
325	LIB3602-019-Q6-K1-B8	730557	BLASTX	348	1.00E-32	64	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
326	LIB3602-043-Q6-K1-D3	730557	BLASTX	316	6.00E-29	61	sativum] 60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
327	LIB3602-046-Q6-K1-A4	730557	BLASTX	316	6.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
328	LIB3602-061-Q6-K1-G10	730557	BLASTX	316	6.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
329	LIB3602-074-Q1-K1-G5	730557	BLASTX	316	6.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
330	LIB3602-062-Q6-K1-F4	730557	BLASTX	316	6.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
331	LIB3602-008-Q6-K1-C9	730557	BLASTX	316	6.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
332	LIB3602-022-Q6-K1-D8	730557	BLASTX	316	6.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
333	LIB3602-076-Q6-K6-D11	730557	BLASTX	316	7.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
334	LIB3602-011-Q6-K1-H4	730557	BLASTX	316	7.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
335	LIB3602-041-Q6-K1-F12	730557	BLASTX	316	7.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
336	LIB3602-028-Q6-K1-H4	730557	BLASTX	316	7.00E-29	61	60S RIBOSOMAL PROTEIN L34 >gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum]
337	LIB3602-063-Q1-K6-H3	730557	BLASTX	314	1.00E-28	57	60S RIBOSOMAL PROTEIN L34

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
338	LIB3602-074-Q1-K1-B3	730557	BLASTX	311	2.00E-28	60	>gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum] 60S RIBOSOMAL PROTEIN L34
339	LIB3602-087-Q6-K1-D4	730557	BLASTX	247	2.00E-22	55	>gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum] 60S RIBOSOMAL PROTEIN L34
340	LIB3602-119-Q1-K1-G1	730557	BLASTX	248	2.00E-21	54	>gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum] 60S RIBOSOMAL PROTEIN L34
341	LIB3602-041-Q6-K1-C10	730557	BLASTX	229	8.00E-19	52	>gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum] 60S RIBOSOMAL PROTEIN L34
342	LIB3602-069-Q1-K1-B3	730557	BLASTX	226	2.00E-18	57	>gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum] 60S RIBOSOMAL PROTEIN L34
343	LIB3602-085-Q6-K1-D11	730557	BLASTX	189	4.00E-14	51	>gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum] 60S RIBOSOMAL PROTEIN L34
344	LIB3602-102-Q1-K1-E11	730557	BLASTX	150	6.00E-10	78	>gi 2119150 pir S60476 ribosomal protein L34, cytosolic - garden pea >gi 498908 gb AAA86953.1 (U10047) ribosomal protein L34 homolog [Pisum sativum] 60S RIBOSOMAL PROTEIN L34
345	LIB3602-067-Q1-K1-E6	2894306	BLASTX	338	2.00E-31	46	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
346	LIB3602-023-Q6-K1-C11	2894306	BLASTX	337	2.00E-31	47	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
347	LIB3602-007-Q1-K1-C11	2894306	BLASTX	338	3.00E-31	46	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
348	LIB3602-094-Q6-K6-E10	2894306	BLASTX	337	3.00E-31	47	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
349	LIB3602-041-Q6-K1-B5	2894306	BLASTX	337	3.00E-31	47	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
350	LIB3602-062-Q6-K1-G10	2894306	BLASTX	317	6.00E-29	45	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
351	LIB3602-113-Q1-K1-F8	2894306	BLASTX	271	1.00E-23	50	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
352	LIB3602-020-Q6-K1-E6	2894306	BLASTX	253	2.00E-21	50	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
353	LIB3602-046-Q6-K1-F2	2894306	BLASTX	249	4.00E-21	50	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
354	LIB3602-101-Q1-K1-H7	2894306	BLASTX	213	1.00E-19	47	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
355	LIB3602-039-Q6-K1-H3	2894306	BLASTX	218	2.00E-17	48	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
356	LIB3602-115-Q1-K1-H6	2894306	BLASTX	217	3.00E-17	47	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
357	LIB3602-002-P1-K6-C12	2894306	BLASTX	215	4.00E-17	49	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
358	LIB3602-045-Q6-K1-A12	2894306	BLASTX	215	4.00E-17	49	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
359	LIB3602-018-Q6-K1-G11	2894306	BLASTX	210	2.00E-16	50	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
360	LIB3602-063-Q1-K6-D10	2894306	BLASTX	208	3.00E-16	50	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
361	LIB3602-090-Q6-K6-D11	2894306	BLASTX	208	3.00E-16	50	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
362	LIB3602-094-Q6-K6-G4	2894306	BLASTX	208	3.00E-16	50	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
363	LIB3602-066-Q1-K6-C10	2894306	BLASTX	208	3.00E-16	50	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
364	LIB3602-100-Q1-K1-F12	2894306	BLASTX	203	8.00E-16	79	(AJ223329) ubiquitin extension protein [Nicotiana tabacum]
365	LIB3602-060-Q6-K1-F12	4204192	BLASTX	461	6.00E-46	82	(AB008095) ribosomal protein L41 [Candida maltosa]
366	LIB3602-032-Q6-K1-D4	4204192	BLASTX	433	9.00E-43	82	(AB008095) ribosomal protein L41 [Candida maltosa]
367	LIB3602-055-Q6-K1-B3	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
368	LIB3602-101-Q1-K1-F11	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
369	LIB3602-061-Q6-K1-F1	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
370	LIB3602-041-Q6-K1-C7	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
371	LIB3602-004-Q1-K1-G6	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
372	LIB3602-009-Q6-K1-H11	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
373	LIB3602-012-Q6-K1-A5	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
374	LIB3602-013-Q6-K1-F7	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
375	LIB3602-023-Q6-K1-H12	4204192	BLASTX	433	1.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
376	LIB3602-025-Q6-K1-C11	4204192	BLASTX	428	5.00E-42	82	(AB008095) ribosomal protein L41 [Candida maltosa]
377	LIB3602-102-Q1-K1-E1	4204192	BLASTX	424	1.00E-41	82	(AB008095) ribosomal protein L41 [Candida maltosa]
378	LIB3602-041-Q6-K1-E6	4204192	BLASTX	424	1.00E-41	80	(AB008095) ribosomal protein L41 [Candida maltosa]
379	LIB3602-038-Q6-K1-F4	4204192	BLASTX	424	2.00E-41	82	(AB008095) ribosomal protein L41 [Candida maltosa]
380	LIB3602-065-Q1-K6-A7	4204192	BLASTX	418	1.00E-40	80	(AB008095) ribosomal protein L41 [Candida maltosa]
381	LIB3602-051-Q6-K1-H9	4204192	BLASTX	408	1.00E-39	79	(AB008095) ribosomal protein L41 [Candida maltosa]
382	LIB3602-085-Q6-K1-H4	4204192	BLASTX	397	2.00E-38	79	(AB008095) ribosomal protein L41 [Candida maltosa]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
383	LIB3602-067-Q1-K1-E8	4204192	BLASTX	397	2.00E-38	79	(AB008095) ribosomal protein L41 [Candida maltosa]
384	LIB3602-108-Q1-K1-E12	4204192	BLASTX	205	2.00E-27	75	(AB008095) ribosomal protein L41 [Candida maltosa]
385	LIB3602-008-Q6-K1-F7	464707	BLASTX	582	4.00E-60	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
386	LIB3602-039-Q6-K1-C9	464707	BLASTX	582	5.00E-60	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
387	LIB3602-070-Q1-K1-C1	464707	BLASTX	582	5.00E-60	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
388	LIB3602-038-Q6-K1-D2	464707	BLASTX	582	5.00E-60	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
389	LIB3602-105-Q1-K1-D4	464707	BLASTX	582	5.00E-60	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
390	LIB3602-076-Q6-K6-C7	464707	BLASTX	582	6.00E-60	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
391	LIB3602-112-Q1-K1-G5	464707	BLASTX	582	6.00E-60	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
392	LIB3602-093-Q6-K6-H10	464707	BLASTX	565	6.00E-58	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
393	LIB3602-057-Q6-K1-G6	464707	BLASTX	457	2.00E-54	80	>gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido 40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
394	LIB3602-107-Q1-K1-F3	464707	BLASTX	481	7.00E-48	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
395	LIB3602-038-Q6-K1-D3	464707	BLASTX	470	7.00E-47	75	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
396	LIB3602-109-Q1-K1-G3	464707	BLASTX	460	9.00E-46	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
397	LIB3602-071-Q1-K1-C10	464707	BLASTX	421	4.00E-41	80	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
398	LIB3602-060-Q6-K1-C12	464707	BLASTX	414	1.00E-40	82	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
399	LIB3602-087-Q6-K1-B11	464707	BLASTX	367	8.00E-35	75	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
400	LIB3602-104-Q1-K1-H10	464707	BLASTX	342	7.00E-32	55	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
401	LIB3602-014-Q6-K1-C1	464707	BLASTX	340	9.00E-32	83	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
402	LIB3602-037-Q6-K1-D10	464707	BLASTX	310	3.00E-28	87	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
403	LIB3602-054-Q6-K1-B12	464707	BLASTX	217	2.00E-17	88	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
404	LIB3602-108-Q1-K1-E5	464707	BLASTX	150	9.00E-10	93	40S RIBOSOMAL PROTEIN S18 >gi 480908 pir S37496 ribosomal protein S18.A, cytosolic - Arabidopsis thaliana >gi 405613 emb CAA80684.1 (Z23165) ribosomal protein S18A [Arabidopsis thaliana] >gi 434343 emb CAA82273.1 (Z28701) S18 ribosomal protein [Arabido
405	LIB3602-094-Q6-K6-G9	7413650	BLASTX	309	4.00E-28	55	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
406	LIB3602-091-Q6-K6-G9	7413650	BLASTX	309	4.00E-28	55	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
407	LIB3602-055-Q6-K1-F5	7413650	BLASTX	309	4.00E-28	55	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
408	LIB3602-079-Q6-K6-G1	7413650	BLASTX	309	4.00E-28	55	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
409	LIB3602-012-Q6-K1-C9	7413650	BLASTX	309	4.00E-28	55	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
410	LIB3602-032-Q6-K1-C9	7413650	BLASTX	298	8.00E-27	55	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
411	LIB3602-104-Q1-K1-E5	7413650	BLASTX	290	6.00E-26	54	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
412	LIB3602-014-Q6-K1-E12	7413650	BLASTX	288	1.00E-25	66	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
413	LIB3602-090-Q6-K6-G2	7413650	BLASTX	286	2.00E-25	53	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
414	LIB3602-058-Q6-K1-H4	7413650	BLASTX	282	4.00E-25	65	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
415	LIB3602-094-Q6-K6-G12	7413650	BLASTX	271	1.00E-23	51	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
416	LIB3602-085-Q6-K1-G11	7413650	BLASTX	259	3.00E-22	62	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
417	LIB3602-043-Q6-K1-E8	7413650	BLASTX	245	6.00E-21	62	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
418	LIB3602-039-Q6-K1-B1	7413650	BLASTX	241	2.00E-20	62	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
419	LIB3602-114-Q1-K1-A4	7413650	BLASTX	231	4.00E-19	59	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
420	LIB3602-043-Q6-K1-H6	7413650	BLASTX	223	3.00E-18	60	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
421	LIB3602-022-Q6-K1-B4	7413650	BLASTX	219	6.00E-18	60	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
422	LIB3602-119-Q1-K1-A4	7413650	BLASTX	143	3.00E-09	68	(AL162971) ribosomal protein L35-like [Arabidopsis thaliana]
423	LIB3602-105-Q1-K1-H2	1350976	BLASTX	813	4.00E-87	78	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
424	LIB3602-089-Q6-K6-D7	1350976	BLASTX	721	3.00E-76	80	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
425	LIB3602-118-Q1-K1-G8	1350976	BLASTX	515	2.00E-70	78	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
426	LIB3602-012-Q6-K1-G12	1350976	BLASTX	633	5.00E-66	77	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
427	LIB3602-112-Q1-K1-E9	1350976	BLASTX	539	6.00E-55	78	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
428	LIB3602-003-Q1-K1-G12	1350976	BLASTX	507	3.00E-51	77	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
429	LIB3602-120-Q1-K1-F12	1350976	BLASTX	325	2.00E-50	74	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
430	LIB3602-029-Q6-K1-H11	1350976	BLASTX	491	2.00E-49	76	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
431	LIB3602-028-Q6-K1-G9	1350976	BLASTX	418	8.00E-41	75	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
432	LIB3602-101-Q1-K1-C8	1350976	BLASTX	413	2.00E-40	75	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
433	LIB3602-017-Q6-K1-B7	1350976	BLASTX	409	9.00E-40	75	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
434	LIB3602-004-Q1-K1-H8	1350976	BLASTX	293	3.00E-26	72	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
435	LIB3602-046-Q6-K1-E5	1350976	BLASTX	278	2.00E-24	71	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
436	LIB3602-020-Q6-K1-D12	1350976	BLASTX	257	4.00E-22	72	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
437	LIB3602-003-Q1-K1-C12	1350976	BLASTX	245	1.00E-20	74	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
438	LIB3602-111-Q1-K1-B7	1350976	BLASTX	243	2.00E-20	74	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
439	LIB3602-021-Q6-K1-C7	1350976	BLASTX	172	2.00E-12	75	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
440	LIB3602-032-Q6-K1-E7	1350976	BLASTX	155	3.00E-10	75	40S RIBOSOMAL PROTEIN S2 >gi 939718 gb AAA74095.1 (U30454) ribosomal protein S2 [Urechis caupo]
441	LIB3602-059-Q6-K1-C5	400991	BLASTX	450	1.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
442	LIB3602-044-Q6-K1-A10	400991	BLASTX	450	1.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
443	LIB3602-041-Q6-K1-F10	400991	BLASTX	450	1.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
444	LIB3602-077-Q6-K6-H3	400991	BLASTX	450	1.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
445	LIB3602-078-Q6-K6-D10	400991	BLASTX	450	1.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
446	LIB3602-010-Q6-K1-C8	400991	BLASTX	450	1.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
447	LIB3602-029-Q6-K1-D9	400991	BLASTX	450	1.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
448	LIB3602-068-Q1-K1-C5	400991	BLASTX	450	2.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
449	LIB3602-053-Q6-K1-B9	400991	BLASTX	444	7.00E-44	66	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
450	LIB3602-067-Q1-K1-A7	400991	BLASTX	428	5.00E-42	64	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
451	LIB3602-022-Q6-K1-G9	400991	BLASTX	426	7.00E-42	64	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
452	LIB3602-100-Q1-K1-C9	400991	BLASTX	412	4.00E-40	63	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
453	LIB3602-038-Q6-K1-H9	400991	BLASTX	408	7.00E-40	70	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
454	LIB3602-101-Q1-K1-B2	400991	BLASTX	287	5.00E-39	71	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
455	LIB3602-071-Q1-K1-C7	400991	BLASTX	209	2.00E-30	58	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
456	LIB3602-101-Q1-K1-H3	400991	BLASTX	235	1.00E-19	64	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
457	LIB3602-086-Q6-K1-E7	400991	BLASTX	231	8.00E-19	45	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
458	LIB3602-006-Q1-K1-E9	400991	BLASTX	224	2.00E-18	55	60S RIBOSOMAL PROTEIN L27 >gi 282737 pir S26612 ribosomal protein L27.e, cytosolic - green alga (Pyrobotrys stellata) >gi 18267 emb CAA48289.1 (X68202) ribosomal protein L27 [Pyrobotrys stellata]
459	LIB3602-083-Q6-K6-A8	6939227	BLASTX	384	7.00E-37	66	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
460	LIB3602-070-Q1-K1-H2	6939227	BLASTX	384	7.00E-37	66	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
461	LIB3602-029-Q6-K1-E5	6939227	BLASTX	384	7.00E-37	66	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
462	LIB3602-058-Q6-K1-C8	6939227	BLASTX	384	7.00E-37	66	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
463	LIB3602-016-Q6-K1-A11	6939227	BLASTX	384	7.00E-37	66	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
464	LIB3602-012-Q6-K1-G11	6939227	BLASTX	384	7.00E-37	66	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
465	LIB3602-019-Q6-K1-H1	6939227	BLASTX	382	7.00E-37	64	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
466	LIB3602-065-Q1-K6-D10	6939227	BLASTX	384	1.00E-36	66	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
467	LIB3602-018-Q6-K1-H7	6939227	BLASTX	375	7.00E-36	65	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
468	LIB3602-109-Q1-K1-A8	6939227	BLASTX	363	2.00E-34	61	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
469	LIB3602-039-Q6-K1-B11	6939227	BLASTX	348	1.00E-32	63	(AC020579) putative ribosomal protein [Arabidopsis thaliana]

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
470	LIB3602-100-Q1-K1-H2	6939227	BLASTX	284	3.00E-25	53	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
471	LIB3602-058-Q6-K1-B9	6939227	BLASTX	207	2.00E-16	64	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
472	LIB3602-091-Q6-K6-G11	6939227	BLASTX	169	3.00E-15	54	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
473	LIB3602-115-Q1-K1-B6	6939227	BLASTX	169	3.00E-15	54	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
474	LIB3602-088-Q6-K6-B6	6939227	BLASTX	169	3.00E-15	54	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
475	LIB3602-052-Q6-K1-D2	6939227	BLASTX	185	6.00E-14	64	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
476	LIB3602-057-Q6-K1-F11	6939227	BLASTX	184	1.00E-13	64	(AC020579) putative ribosomal protein [Arabidopsis thaliana]
477	LIB3602-013-Q6-K1-C10	1710521	BLASTX	405	2.00E-39	63	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
478	LIB3602-027-Q6-K1-F6	1710521	BLASTX	393	4.00E-38	62	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
479	LIB3602-013-Q6-K1-D2	1710521	BLASTX	367	7.00E-35	60	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
480	LIB3602-025-Q6-K1-G7	1710521	BLASTX	367	7.00E-35	60	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
481	LIB3602-001-P1-K6-B9	1710521	BLASTX	367	8.00E-35	60	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
482	LIB3602-001-P1-K6-D12	1710521	BLASTX	367	8.00E-35	60	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
483	LIB3602-056-Q6-K1-F11	1710521	BLASTX	361	3.00E-34	59	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
484	LIB3602-081-Q6-K6-A4	1710521	BLASTX	353	4.00E-33	59	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
485	LIB3602-019-Q6-K1-G2	1710521	BLASTX	351	5.00E-33	58	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
486	LIB3602-112-Q1-K1-B8	1710521	BLASTX	328	3.00E-30	57	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
487	LIB3602-100-Q1-K1-E9	1710521	BLASTX	220	2.00E-29	58	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
488	LIB3602-045-Q6-K1-B7	1710521	BLASTX	258	3.00E-22	56	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
489	LIB3602-030-Q6-K1-F12	1710521	BLASTX	258	4.00E-22	56	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
490	LIB3602-004-Q1-K1-G8	1710521	BLASTX	235	2.00E-19	56	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
491	LIB3602-108-Q1-K1-C2	1710521	BLASTX	173	3.00E-12	57	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
492	LIB3602-019-Q6-K1-G3	1710521	BLASTX	161	3.00E-11	44	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
493	LIB3602-028-Q6-K1-C6	1710521	BLASTX	161	5.00E-11	56	60S RIBOSOMAL PROTEIN L24 >gi 7440778 pir T06178 ribosomal protein L24 - barley >gi 1154859 emb CAA63960.1 (X94296) L24 ribosomal protein [Hordeum vulgare]
494	LIB3602-043-Q6-K1-G10	5902584	BLASTX	494	8.00E-50	71	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
495	LIB3602-060-Q6-K1-H10	5902584	BLASTX	467	1.00E-46	72	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
496	LIB3602-054-Q6-K1-B1	5902584	BLASTX	427	5.00E-42	78	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
497	LIB3602-014-Q6-K1-D12	5902584	BLASTX	419	4.00E-41	79	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
498	LIB3602-080-Q6-K6-F4	5902584	BLASTX	354	6.00E-37	77	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
499	LIB3602-058-Q6-K1-H6	5902584	BLASTX	375	6.00E-36	78	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
500	LIB3602-065-Q1-K6-F2	5902584	BLASTX	368	4.00E-35	76	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
501	LIB3602-092-Q6-K6-F12	5902584	BLASTX	354	4.00E-34	77	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
502	LIB3602-079-Q6-K6-F9	5902584	BLASTX	354	1.00E-33	77	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
503	LIB3602-088-Q6-K6-F3	5902584	BLASTX	350	7.00E-33	75	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
504	LIB3602-104-Q1-K1-E8	5902584	BLASTX	347	1.00E-32	76	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
505	LIB3602-064-Q1-K6-H7	5902584	BLASTX	346	1.00E-32	77	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
506	LIB3602-103-Q1-K1-E2	5902584	BLASTX	225	2.00E-32	82	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
507	LIB3602-093-Q6-K6-D7	5902584	BLASTX	271	7.00E-29	71	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
508	LIB3602-050-Q6-K1-A10	5902584	BLASTX	286	2.00E-25	76	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
509	LIB3602-077-Q6-K6-H7	5902584	BLASTX	253	7.00E-22	78	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]
510	LIB3602-036-Q6-K1-F9	5902584	BLASTX	159	6.00E-11	87	(AF110780) oxygen-evolving enhancer protein 1 precursor [Volvox carteri f. nagariensis]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
511	LIB3602-030-Q6-K1-G9	6831602	BLASTX	408	8.00E-40	83	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
512	LIB3602-014-Q6-K1-H8	6831602	BLASTX	408	8.00E-40	83	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
513	LIB3602-034-Q6-K1-E1	6831602	BLASTX	408	8.00E-40	83	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
514	LIB3602-017-Q6-K1-F11	6831602	BLASTX	387	2.00E-37	83	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
515	LIB3602-027-Q6-K1-H10	6831602	BLASTX	382	7.00E-37	83	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
516	LIB3602-035-Q1-K1-E1	6831602	BLASTX	378	3.00E-36	82	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
517	LIB3602-069-Q1-K1-C12	6831602	BLASTX	378	3.00E-36	82	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
518	LIB3602-087-Q6-K1-E1	6831602	BLASTX	378	3.00E-36	82	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
519	LIB3602-021-Q6-K1-D6	6831602	BLASTX	371	1.00E-35	84	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
520	LIB3602-021-Q6-K1-B12	6831602	BLASTX	369	2.00E-35	81	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
521	LIB3602-019-Q6-K1-A12	6831602	BLASTX	365	7.00E-35	80	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
522	LIB3602-021-Q6-K1-F9	6831602	BLASTX	327	1.00E-30	81	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
523	LIB3602-067-Q1-K1-D5	6831602	BLASTX	182	1.00E-25	92	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
524	LIB3602-054-Q6-K1-F9	6831602	BLASTX	275	2.00E-24	79	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
525	LIB3602-060-Q6-K1-D12	6831602	BLASTX	239	3.00E-20	78	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
526	LIB3602-043-Q6-K1-B11	6831602	BLASTX	207	8.00E-17	64	(AF127042) 60S ribosomal protein L37a [Gossypium hirsutum] 60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
527	LIB3602-011-Q6-K1-A6	6831602	BLASTX	204	8.00E-16	53	60S RIBOSOMAL PROTEIN L37A >gi 4741896 gb AAD28753.1 AF127042_1 (AF127042) 60S ribosomal protein L37a [Gossypium hirsutum]
528	LIB3602-102-Q1-K1-H6	6174959	BLASTX	441	3.00E-50	71	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
529	LIB3602-056-Q6-K1-B4	6174959	BLASTX	488	4.00E-49	69	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
530	LIB3602-113-Q1-K1-B5	6174959	BLASTX	488	6.00E-49	70	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
531	LIB3602-070-Q1-K1-F5	6174959	BLASTX	484	2.00E-48	70	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
532	LIB3602-093-Q6-K6-E5	6174959	BLASTX	484	2.00E-48	70	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
533	LIB3602-012-Q6-K1-C7	6174959	BLASTX	484	2.00E-48	70	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
534	LIB3602-112-Q1-K1-B5	6174959	BLASTX	484	2.00E-48	70	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
535	LIB3602-116-Q1-K1-B6	6174959	BLASTX	470	4.00E-47	71	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
536	LIB3602-002-P1-K6-G8	6174959	BLASTX	452	8.00E-45	72	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
537	LIB3602-059-Q6-K1-D12	6174959	BLASTX	331	3.00E-41	65	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
538	LIB3602-038-Q6-K1-G10	6174959	BLASTX	416	1.00E-40	73	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
539	LIB3602-042-Q6-K1-G2	6174959	BLASTX	408	1.00E-39	68	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
540	LIB3602-120-Q1-K1-B5	6174959	BLASTX	292	1.00E-35	68	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
541	LIB3602-114-Q1-K1-A1	6174959	BLASTX	350	4.00E-33	66	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
542	LIB3602-072-Q1-K1-E9	6174959	BLASTX	274	3.00E-32	74	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
543	LIB3602-006-Q1-K1-F11	6174959	BLASTX	199	4.00E-15	41	60S RIBOSOMAL PROTEIN L9 >gi 7440702 pir T03761 probable ribosomal protein L9 - rice >gi 2058273 dbj BAA19798.1 (D83527) YK426 [Oryza sativa]
544	LIB3602-027-Q6-K1-H11	7440314	BLASTX	425	1.00E-41	60	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
545	LIB3602-089-Q6-K6-E9	7440314	BLASTX	425	1.00E-41	60	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
546	LIB3602-079-Q6-K6-A6	7440314	BLASTX	422	3.00E-41	60	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
547	LIB3602-109-Q1-K1-B1	7440314	BLASTX	419	6.00E-41	61	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
548	LIB3602-009-Q6-K1-F5	7440314	BLASTX	409	8.00E-40	75	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
549	LIB3602-043-Q6-K1-B10	7440314	BLASTX	409	8.00E-40	75	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
550	LIB3602-037-Q6-K1-D12	7440314	BLASTX	407	1.00E-39	74	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
551	LIB3602-100-Q1-K1-D6	7440314	BLASTX	404	3.00E-39	74	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
552	LIB3602-064-Q1-K6-C9	7440314	BLASTX	361	4.00E-36	58	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
553	LIB3602-072-Q1-K1-G11	7440314	BLASTX	356	5.00E-36	57	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
554	LIB3602-101-Q1-K1-C1	7440314	BLASTX	323	1.00E-35	71	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
555	LIB3602-083-Q6-K6-A5	7440314	BLASTX	336	3.00E-31	56	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
556	LIB3602-084-Q6-K1-B6	7440314	BLASTX	330	2.00E-30	54	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
557	LIB3602-109-Q1-K1-A5	7440314	BLASTX	195	7.00E-24	76	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1 (AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
558	LIB3602-064-Q1-K6-F3	7440314	BLASTX	197	4.00E-18	44	ribosomal protein S10, cytosolic - Arabidopsis thaliana >gi 4539292 emb CAB39595.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							(AL049480) putative ribosomal protein S10 [Arabidopsis thaliana] >gi 7269424 emb CAB81384.1 (AL161563) putative ribosomal protein S10 [Arabidopsis thaliana]
559	LIB3602-008-Q6-K1-C11	6683481	BLASTX	566	3.00E-58	81	(AB018560) wrp15a [Citrullus lanatus]
560	LIB3602-025-Q6-K1-C10	6683481	BLASTX	566	3.00E-58	81	(AB018560) wrp15a [Citrullus lanatus]
561	LIB3602-069-Q1-K1-B4	6683481	BLASTX	438	7.00E-52	79	(AB018560) wrp15a [Citrullus lanatus]
562	LIB3602-068-Q1-K1-B4	6683481	BLASTX	438	8.00E-52	79	(AB018560) wrp15a [Citrullus lanatus]
563	LIB3602-103-Q1-K1-C2	6683481	BLASTX	510	1.00E-51	81	(AB018560) wrp15a [Citrullus lanatus]
564	LIB3602-105-Q1-K1-B5	6683481	BLASTX	438	8.00E-51	79	(AB018560) wrp15a [Citrullus lanatus]
565	LIB3602-084-Q6-K1-B2	6683481	BLASTX	438	9.00E-50	79	(AB018560) wrp15a [Citrullus lanatus]
566	LIB3602-047-Q6-K1-D6	6683481	BLASTX	443	8.00E-44	82	(AB018560) wrp15a [Citrullus lanatus]
567	LIB3602-077-Q6-K6-H5	6683481	BLASTX	438	3.00E-43	79	(AB018560) wrp15a [Citrullus lanatus]
568	LIB3602-055-Q6-K1-E12	6683481	BLASTX	428	4.00E-42	82	(AB018560) wrp15a [Citrullus lanatus]
569	LIB3602-071-Q1-K1-F3	6683481	BLASTX	419	5.00E-41	79	(AB018560) wrp15a [Citrullus lanatus]
570	LIB3602-074-Q1-K1-E7	6683481	BLASTX	341	4.00E-35	75	(AB018560) wrp15a [Citrullus lanatus]
571	LIB3602-086-Q6-K1-H6	6683481	BLASTX	258	2.00E-32	66	(AB018560) wrp15a [Citrullus lanatus]
572	LIB3602-077-Q6-K6-D5	6683481	BLASTX	319	2.00E-29	70	(AB018560) wrp15a [Citrullus lanatus]
573	LIB3602-023-Q6-K1-G5	115778	BLASTX	653	2.00E-68	72	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
574	LIB3602-094-Q6-K6-F3	115778	BLASTX	653	3.00E-68	71	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
575	LIB3602-015-Q6-K1-G9	115778	BLASTX	536	1.00E-54	70	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
576	LIB3602-008-Q6-K1-A6	115778	BLASTX	495	7.00E-50	70	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
577	LIB3602-013-Q6-K1-H5	115778	BLASTX	478	8.00E-48	70	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
578	LIB3602-090-Q6-K6-B4	115778	BLASTX	471	6.00E-47	71	CHLOROPHYLL A-B BINDING PROTEIN 1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
579	LIB3602-105-Q1-K1-F2	115778	BLASTX	464	4.00E-46	71	PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140 CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
580	LIB3602-025-Q6-K1-H12	115778	BLASTX	459	1.00E-45	71	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
581	LIB3602-105-Q1-K1-B7	115778	BLASTX	431	2.00E-42	70	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
582	LIB3602-029-Q6-K1-B7	115778	BLASTX	409	9.00E-40	70	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
583	LIB3602-050-Q6-K1-B9	115778	BLASTX	392	7.00E-38	71	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
584	LIB3602-027-Q6-K1-A7	115778	BLASTX	364	2.00E-34	61	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
585	LIB3602-018-Q6-K1-A1	115778	BLASTX	319	2.00E-33	59	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
586	LIB3602-115-Q1-K1-D2	115778	BLASTX	151	1.00E-13	63	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll a/b-binding

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							protein precursor - white mustard >gi 21138 emb CAA34459.1 (X16436) chlorophyll a/b-binding protein (AA 1-266) [Sinapis alba] >gi 21140
587	LIB3602-103-Q1-K1-C4	548852	BLASTX	303	2.00E-27	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
588	LIB3602-037-Q6-K1-C5	548852	BLASTX	303	2.00E-27	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
589	LIB3602-053-Q6-K1-C7	548852	BLASTX	303	2.00E-27	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
590	LIB3602-066-Q1-K6-C8	548852	BLASTX	303	2.00E-27	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
591	LIB3602-030-Q6-K1-G1	548852	BLASTX	303	2.00E-27	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
592	LIB3602-063-Q1-K6-D8	548852	BLASTX	298	7.00E-27	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
593	LIB3602-093-Q6-K6-A11	548852	BLASTX	298	1.00E-26	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
594	LIB3602-034-Q6-K1-D2	548852	BLASTX	291	4.00E-26	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
595	LIB3602-104-Q1-K1-A11	548852	BLASTX	286	3.00E-25	61	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
596	LIB3602-048-Q6-K1QA-H5	548852	BLASTX	257	4.00E-22	66	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
597	LIB3602-016-Q6-K1-H5	548852	BLASTX	254	9.00E-22	65	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
598	LIB3602-115-Q1-K1-H12	548852	BLASTX	229	1.00E-21	60	sativa] 40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
599	LIB3602-073-Q1-K1-G7	548852	BLASTX	240	4.00E-20	63	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
600	LIB3602-101-Q1-K1-C4	548852	BLASTX	145	6.00E-20	69	40S RIBOSOMAL PROTEIN S21 >gi 481227 pir S38357 ribosomal protein S21, cytosolic - rice >gi 303839 dbj BAA02158.1 (D12633) 40S subunit ribosomal protein [Oryza sativa]
601	LIB3602-115-Q1-K1-D5	115832	BLASTX	264	5.00E-23	87	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
602	LIB3602-095-Q6-K6-F1	115832	BLASTX	266	6.00E-23	73	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
603	LIB3602-009-Q6-K1-F11	115832	BLASTX	261	2.00E-22	75	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
604	LIB3602-009-Q6-K1-E8	115832	BLASTX	261	2.00E-22	75	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
605	LIB3602-034-Q6-K1-A4	115832	BLASTX	258	3.00E-22	87	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
606	LIB3602-063-Q1-K6-E1	115832	BLASTX	258	5.00E-22	69	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
607	LIB3602-035-Q1-K1-A4	115832	BLASTX	244	2.00E-20	86	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
608	LIB3602-061-Q6-K1-A5	115832	BLASTX	205	6.00E-16	71	chlorophyll binding protein [Physcomitrella patens] CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
609	LIB3602-025-Q6-K1-B2	115832	BLASTX	205	7.00E-16	71	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
610	LIB3602-053-Q6-K1-A4	115832	BLASTX	178	6.00E-13	86	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
611	LIB3602-018-Q6-K1-G6	115832	BLASTX	174	1.00E-12	86	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
612	LIB3602-006-Q1-K1-B9	115832	BLASTX	145	2.00E-10	62	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
613	LIB3602-082-Q6-K6-E4	115832	BLASTX	143	7.00E-09	65	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 81414 pir JS0171 chlorophyll a/b-binding protein precursor - moss (Physcomitrella patens) >gi 169020 gb AAA33636.1 (M23532) major chlorophyll binding protein [Physcomitrella patens]
614	LIB3602-073-Q1-K1-G12	4262180	BLASTX	823	3.00E-88	86	(AC005508) 29621 [Arabidopsis thaliana]
615	LIB3602-113-Q1-K1-H1	4262180	BLASTX	822	4.00E-88	84	(AC005508) 29621 [Arabidopsis thaliana]
616	LIB3602-106-Q1-K1-A5	4262180	BLASTX	807	2.00E-86	84	(AC005508) 29621 [Arabidopsis thaliana]
617	LIB3602-007-Q1-K1-F8	4262180	BLASTX	791	2.00E-84	86	(AC005508) 29621 [Arabidopsis thaliana]
618	LIB3602-070-Q1-K1-B1	4262180	BLASTX	732	1.00E-77	80	(AC005508) 29621 [Arabidopsis thaliana]
619	LIB3602-007-Q1-K1-B10	4262180	BLASTX	701	5.00E-74	88	(AC005508) 29621 [Arabidopsis thaliana]
620	LIB3602-032-Q6-K1-E1	4262180	BLASTX	701	5.00E-74	88	(AC005508) 29621 [Arabidopsis thaliana]
621	LIB3602-047-Q6-K1-D2	4262180	BLASTX	701	5.00E-74	88	(AC005508) 29621 [Arabidopsis thaliana]
622	LIB3602-111-Q1-K1-G4	4262180	BLASTX	543	1.00E-68	86	(AC005508) 29621 [Arabidopsis thaliana]
623	LIB3602-054-Q6-K1-B7	4262180	BLASTX	648	7.00E-68	81	(AC005508) 29621 [Arabidopsis thaliana]
624	LIB3602-102-Q1-K1-D8	4262180	BLASTX	507	8.00E-65	87	(AC005508) 29621 [Arabidopsis thaliana]
625	LIB3602-120-Q1-K1-H1	4262180	BLASTX	514	3.00E-52	87	(AC005508) 29621 [Arabidopsis thaliana]
626	LIB3602-119-Q1-K1-B12	4262180	BLASTX	288	1.00E-43	81	(AC005508) 29621 [Arabidopsis thaliana]
627	LIB3602-102-Q1-K1-F9	6984222	BLASTX	572	6.00E-59	75	(AF227979) 40S ribosomal protein S16 [Euphorbia esula]
628	LIB3602-054-Q6-K1-H4	6984222	BLASTX	572	6.00E-59	75	(AF227979) 40S ribosomal protein S16 [Euphorbia esula]
629	LIB3602-018-Q6-K1-E4	6984222	BLASTX	572	7.00E-59	75	(AF227979) 40S ribosomal protein S16 [Euphorbia

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
630	LIB3602-074-Q1-K1-B4	6984222	BLASTX	572	7.00E-59	75	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
631	LIB3602-023-Q6-K1-D4	6984222	BLASTX	572	7.00E-59	75	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
632	LIB3602-051-Q6-K1-E1	6984222	BLASTX	568	2.00E-58	74	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
633	LIB3602-007-Q1-K1-F2	6984222	BLASTX	544	2.00E-55	72	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
634	LIB3602-069-Q1-K1-C5	6984222	BLASTX	523	6.00E-54	73	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
635	LIB3602-070-Q1-K1-D10	6984222	BLASTX	523	6.00E-54	73	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
636	LIB3602-116-Q1-K1-E12	6984222	BLASTX	431	1.00E-53	79	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
637	LIB3602-034-Q6-K1-B1	6984222	BLASTX	510	1.00E-51	69	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
638	LIB3602-034-Q6-K1-A1	6984222	BLASTX	225	1.00E-18	59	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
639	LIB3602-068-Q1-K1-C7	6984222	BLASTX	198	2.00E-15	86	esula] (AF227979) 40S ribosomal protein S16 [Euphorbia
640	LIB3602-104-Q1-K1-E1	2440160	BLASTX	279	2.00E-24	50	(Y14836) beta-galactosidase [Phagemid cloning
641	LIB3602-112-Q1-K1-D6	2440160	BLASTX	274	8.00E-24	53	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
642	LIB3602-061-Q6-K1-H10	2440160	BLASTX	242	3.00E-20	56	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
643	LIB3602-094-Q6-K6-C4	2440160	BLASTX	219	2.00E-17	41	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
644	LIB3602-004-Q1-K1-F8	2440160	BLASTX	216	4.00E-17	43	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
645	LIB3602-076-Q6-K6-F12	2440160	BLASTX	200	4.00E-15	40	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
646	LIB3602-041-Q6-K1-B7	2440160	BLASTX	161	5.00E-15	55	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
647	LIB3602-006-Q1-K1-A5	2440160	BLASTX	191	3.00E-14	41	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
648	LIB3602-001-P1-K6-D9	2440160	BLASTX	177	1.00E-12	36	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
649	LIB3602-115-Q1-K1-F9	2440160	BLASTX	172	4.00E-12	36	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
650	LIB3602-036-Q6-K1-E11	2440160	BLASTX	152	1.00E-09	36	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
651	LIB3602-062-Q6-K1-A5	2440160	BLASTX	150	2.00E-09	36	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
652	LIB3602-052-Q6-K1-B3	2440160	BLASTX	144	9.00E-09	38	vector pTZ19U] (Y14836) beta-galactosidase [Phagemid cloning
653	LIB3602-018-Q6-K1-E8	7440313	BLASTX	611	2.00E-63	73	vector pTZ19U] ribosomal protein S6.1, cytosolic - maize
654	LIB3602-104-Q1-K1-H4	7440313	BLASTX	611	2.00E-63	68	>gi 1917019 gb AAB51304.1 (U92045) ribosomal
655	LIB3602-073-Q1-K1-H12	7440313	BLASTX	435	4.00E-53	65	protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
656	LIB3602-107-Q1-K1-H5	7440313	BLASTX	475	2.00E-47	64	>gi 1917019 gb AAB51304.1 (U92045) ribosomal
							protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
657	LIB3602-115-Q1-K1-B8	7440313	BLASTX	463	5.00E-46	56	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
658	LIB3602-004-Q1-K1-G1	7440313	BLASTX	451	7.00E-45	51	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
659	LIB3602-053-Q6-K1-C5	7440313	BLASTX	417	9.00E-41	62	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
660	LIB3602-001-P1-K6-E9	7440313	BLASTX	409	9.00E-40	62	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
661	LIB3602-020-Q6-K1-E3	7440313	BLASTX	386	4.00E-37	60	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
662	LIB3602-012-Q6-K1-E10	7440313	BLASTX	234	2.00E-19	53	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
663	LIB3602-079-Q6-K6-H5	7440313	BLASTX	159	8.00E-17	65	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
664	LIB3602-060-Q6-K1-F7	7440313	BLASTX	154	4.00E-10	64	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
665	LIB3602-119-Q1-K1-G3	7440313	BLASTX	149	2.00E-09	77	>gi 1917019 gb AAB51304.1 (U92045) ribosomal protein S6 RPS6-1 [Zea mays] ribosomal protein S6.1, cytosolic - maize
666	LIB3602-026-Q6-K1-F6	7293042	BLASTX	371	1.00E-35	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
667	LIB3602-068-Q1-K1-D10	7293042	BLASTX	371	2.00E-35	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
668	LIB3602-077-Q6-K6-A6	7293042	BLASTX	371	2.00E-35	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
669	LIB3602-079-Q6-K6-B2	7293042	BLASTX	371	2.00E-35	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
670	LIB3602-105-Q1-K1-D5	7293042	BLASTX	371	2.00E-35	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
671	LIB3602-068-Q1-K1-B9	7293042	BLASTX	371	2.00E-35	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
672	LIB3602-037-Q6-K1-F8	7293042	BLASTX	371	2.00E-35	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
673	LIB3602-027-Q6-K1-D1	7293042	BLASTX	371	2.00E-35	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
674	LIB3602-057-Q6-K1-E9	7293042	BLASTX	364	1.00E-34	79	(AE003498) CG9091 gene product [Drosophila melanogaster]
675	LIB3602-053-Q6-K1-F11	7293042	BLASTX	351	4.00E-33	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
676	LIB3602-053-Q6-K1-F5	7293042	BLASTX	348	6.00E-33	79	(AE003498) CG9091 gene product [Drosophila melanogaster]
677	LIB3602-106-Q1-K1-F5	7293042	BLASTX	245	2.00E-24	82	(AE003498) CG9091 gene product [Drosophila melanogaster]
678	LIB3602-120-Q1-K1-E11	7293042	BLASTX	232	2.00E-19	80	(AE003498) CG9091 gene product [Drosophila melanogaster]
679	LIB3602-055-Q6-K1-A6	445613	BLASTX	542	2.00E-55	75	ribosomal protein L7 [Solanum tuberosum]
680	LIB3602-089-Q6-K6-E7	445613	BLASTX	542	3.00E-55	75	ribosomal protein L7 [Solanum tuberosum]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
681	LIB3602-057-Q6-K1-C4	445613	BLASTX	533	3.00E-54	73	ribosomal protein L7 [Solanum tuberosum]
682	LIB3602-034-Q6-K1-D4	445613	BLASTX	532	3.00E-54	74	ribosomal protein L7 [Solanum tuberosum]
683	LIB3602-059-Q6-K1-G10	445613	BLASTX	521	7.00E-53	73	ribosomal protein L7 [Solanum tuberosum]
684	LIB3602-035-Q1-K1-D4	445613	BLASTX	497	4.00E-50	72	ribosomal protein L7 [Solanum tuberosum]
685	LIB3602-070-Q1-K1-D9	445613	BLASTX	473	3.00E-47	62	ribosomal protein L7 [Solanum tuberosum]
686	LIB3602-061-Q6-K1-F6	445613	BLASTX	442	7.00E-44	71	ribosomal protein L7 [Solanum tuberosum]
687	LIB3602-040-Q6-K1-G8	445613	BLASTX	412	2.00E-40	71	ribosomal protein L7 [Solanum tuberosum]
688	LIB3602-111-Q1-K1-A5	445613	BLASTX	236	8.00E-36	68	ribosomal protein L7 [Solanum tuberosum]
689	LIB3602-040-Q6-K1-A3	445613	BLASTX	349	7.00E-33	70	ribosomal protein L7 [Solanum tuberosum]
690	LIB3602-025-Q6-K1-B5	445613	BLASTX	339	1.00E-31	70	ribosomal protein L7 [Solanum tuberosum]
691	LIB3602-018-Q6-K1-D9	445613	BLASTX	292	3.00E-26	69	ribosomal protein L7 [Solanum tuberosum]
692	LIB3602-047-Q6-K1-B8	6441068	BLASTX	675	5.00E-71	77	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
693	LIB3602-072-Q1-K1-B7	6441068	BLASTX	572	8.00E-59	59	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
694	LIB3602-061-Q6-K1-A1	6441068	BLASTX	564	5.00E-58	71	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
695	LIB3602-113-Q1-K1-G4	6441068	BLASTX	531	5.00E-54	59	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
696	LIB3602-059-Q6-K1-A5	6441068	BLASTX	507	3.00E-51	70	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
697	LIB3602-063-Q1-K6-D4	6441068	BLASTX	505	4.00E-51	70	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
698	LIB3602-046-Q6-K1-B7	6441068	BLASTX	473	2.00E-47	71	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
699	LIB3602-046-Q6-K1-E3	6441068	BLASTX	335	3.00E-31	54	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
700	LIB3602-059-Q6-K1-A6	6441068	BLASTX	202	3.00E-30	60	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
701	LIB3602-107-Q1-K1-H11	6441068	BLASTX	297	1.00E-26	48	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
702	LIB3602-093-Q6-K6-D10	6441068	BLASTX	292	1.00E-26	73	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
703	LIB3602-020-Q6-K1-B6	6441068	BLASTX	177	1.00E-24	69	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
704	LIB3602-057-Q6-K1-F4	6441068	BLASTX	166	2.00E-22	40	(AU066549) 60S ribosomal protein L4 [Chlamydomonas sp.]
705	LIB3602-071-Q1-K1-D6	6320978	BLASTX	276	4.00E-24	59	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
706	LIB3602-106-Q1-K1-D11	6320978	BLASTX	276	4.00E-24	59	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
707	LIB3602-067-Q1-K1-D10	6320978	BLASTX	276	4.00E-24	59	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
708	LIB3602-084-Q6-K1-A12	6320978	BLASTX	271	1.00E-23	59	>gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
709	LIB3602-053-Q6-K1-A2	6320978	BLASTX	269	1.00E-23	59	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
710	LIB3602-027-Q6-K1-H8	6320978	BLASTX	269	2.00E-23	59	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
711	LIB3602-043-Q6-K1-E5	6320978	BLASTX	269	2.00E-23	59	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
712	LIB3602-041-Q6-K1-C3	6320978	BLASTX	269	3.00E-23	59	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
713	LIB3602-017-Q6-K1-D12	6320978	BLASTX	262	2.00E-22	58	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
714	LIB3602-029-Q6-K1-A2	6320978	BLASTX	260	3.00E-22	57	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia
715	LIB3602-111-Q1-K1-A3	6320978	BLASTX	212	4.00E-19	58	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [Saccharomyces cerevisia

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
716	LIB3602-107-Q1-K1-H9	6320978	BLASTX	195	7.00E-15	59	Ribosomal protein S26B; Rps26bp >gi 730459 sp P39939 R26B_YEAST 40S RIBOSOMAL PROTEIN S26-B >gi 1071981 pir S50634 ribosomal protein S26.e.B, cytosolic - yeast (<i>Saccharomyces cerevisiae</i>) >gi 603370 gb AAC03229.1 (U18916) Rps26bp [<i>Saccharomyces cerevisia</i>
717	LIB3602-090-Q6-K6-H12	3122703	BLASTX	485	1.00E-48	75	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
718	LIB3602-045-Q6-K1-D4	3122703	BLASTX	479	5.00E-48	73	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
719	LIB3602-091-Q6-K6-H12	3122703	BLASTX	479	6.00E-48	74	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
720	LIB3602-055-Q6-K1-D4	3122703	BLASTX	473	2.00E-47	75	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
721	LIB3602-094-Q6-K6-G1	3122703	BLASTX	473	3.00E-47	75	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
722	LIB3602-115-Q1-K1-E5	3122703	BLASTX	473	3.00E-47	75	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
723	LIB3602-114-Q1-K1-H1	3122703	BLASTX	473	3.00E-47	75	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
724	LIB3602-029-Q6-K1-D4	3122703	BLASTX	473	3.00E-47	75	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
725	LIB3602-091-Q6-K6-G1	3122703	BLASTX	473	3.00E-47	75	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
726	LIB3602-111-Q1-K1-H2	3122703	BLASTX	456	3.00E-45	76	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
727	LIB3602-108-Q1-K1-C10	3122703	BLASTX	439	1.00E-44	75	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
728	LIB3602-093-Q6-K6-F1	3122703	BLASTX	201	4.00E-21	47	60S RIBOSOMAL PROTEIN L23A >gi 2641201 gb AAB86852.1 (AF031542) ribosomal protein L23a [<i>Fritillaria agrestis</i>]
729	LIB3602-060-Q6-K1-C10	1173222	BLASTX	565	4.00E-58	71	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (<i>Dunaliella tertiolecta</i>) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [<i>Dunaliella tertiolecta</i>]
730	LIB3602-094-Q6-K6-H2	1173222	BLASTX	519	5.00E-54	78	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (<i>Dunaliella tertiolecta</i>) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [<i>Dunaliella tertiolecta</i>]
731	LIB3602-104-Q1-K1-H7	1173222	BLASTX	519	1.00E-52	78	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (<i>Dunaliella tertiolecta</i>) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [<i>Dunaliella tertiolecta</i>]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
732	LIB3602-111-Q1-K1-H9	1173222	BLASTX	516	2.00E-52	76	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
733	LIB3602-088-Q6-K6-G4	1173222	BLASTX	445	1.00E-47	81	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
734	LIB3602-114-Q1-K1-E2	1173222	BLASTX	446	5.00E-44	80	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
735	LIB3602-088-Q6-K6-C11	1173222	BLASTX	445	6.00E-44	80	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
736	LIB3602-108-Q1-K1-E7	1173222	BLASTX	421	7.00E-43	75	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
737	LIB3602-060-Q6-K1-E9	1173222	BLASTX	418	5.00E-41	68	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
738	LIB3602-090-Q6-K6-H4	1173222	BLASTX	278	2.00E-40	83	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
739	LIB3602-077-Q6-K6-G4	1173222	BLASTX	311	3.00E-28	80	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
740	LIB3602-108-Q1-K1-F11	1173222	BLASTX	297	1.00E-27	62	40S RIBOSOMAL PROTEIN S11 >gi 7440474 pir T10730 ribosomal protein S11 - green alga (Dunaliella tertiolecta) >gi 534959 emb CAA46835.1 (X66036) ribosomal protein S11 [Dunaliella tertiolecta]
741	LIB3602-043-Q6-K1-G12	4038471	BLASTX	313	1.00E-28	74	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
742	LIB3602-011-Q6-K1-D1	4038471	BLASTX	313	2.00E-28	74	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
743	LIB3602-062-Q6-K1-F6	4038471	BLASTX	313	2.00E-28	74	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
744	LIB3602-020-Q6-K1-D6	4038471	BLASTX	303	2.00E-27	88	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
745	LIB3602-055-Q6-K1-B10	4038471	BLASTX	298	8.00E-27	74	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
746	LIB3602-032-Q6-K1-E12	4038471	BLASTX	287	1.00E-25	89	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
747	LIB3602-039-Q6-K1-H9	4038471	BLASTX	259	4.00E-22	90	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
748	LIB3602-056-Q6-K1-C2	4038471	BLASTX	249	4.00E-21	89	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
749	LIB3602-090-Q6-K6-E4	4038471	BLASTX	229	1.00E-18	91	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
750	LIB3602-113-Q1-K1-G9	4038471	BLASTX	206	6.00E-16	90	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
751	LIB3602-055-Q6-K1-B11	4038471	BLASTX	165	3.00E-11	64	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
752	LIB3602-001-P1-K6-F4	4038471	BLASTX	156	4.00E-10	90	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
753	LIB3602-060-Q6-K1-G5	115829	BLASTX	684	5.00E-72	78	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
754	LIB3602-085-Q6-K1-C6	115829	BLASTX	635	3.00E-66	75	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
755	LIB3602-054-Q6-K1-A8	115829	BLASTX	603	1.00E-62	77	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
756	LIB3602-094-Q6-K6-A5	115829	BLASTX	547	5.00E-61	75	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
757	LIB3602-018-Q6-K1-F7	115829	BLASTX	564	6.00E-58	64	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
758	LIB3602-071-Q1-K1-D3	115829	BLASTX	558	4.00E-57	75	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
759	LIB3602-002-P1-K6-D8	115829	BLASTX	451	1.00E-44	75	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
760	LIB3602-051-Q6-K1-C2	115829	BLASTX	358	5.00E-42	74	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
761	LIB3602-111-Q1-K1-E11	115829	BLASTX	297	7.00E-42	75	tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
762	LIB3602-090-Q6-K6-A12	115829	BLASTX	256	5.00E-33	67	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
763	LIB3602-023-Q6-K1-H1	115829	BLASTX	275	3.00E-30	44	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
764	LIB3602-001-P1-K6-D6	115829	BLASTX	315	5.00E-29	77	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99364 pir JW0040 chlorophyll a/b-binding protein 28.5K precursor - green alga (Dunaliella tertiolecta) >gi 167985 gb AAA62772.1 (M60049) 28.5 kDa LHCII apoprotein [Dunaliella ter
765	LIB3602-042-Q6-K1-G9	1172977	BLASTX	716	1.00E-75	74	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
766	LIB3602-042-Q6-K1-G10	1172977	BLASTX	709	8.00E-75	74	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
767	LIB3602-067-Q1-K1-D6	1172977	BLASTX	694	4.00E-73	74	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
768	LIB3602-089-Q6-K6-B5	1172977	BLASTX	688	2.00E-72	73	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
769	LIB3602-084-Q6-K1-A10	1172977	BLASTX	673	1.00E-70	73	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
770	LIB3602-069-Q1-K1-D5	1172977	BLASTX	669	3.00E-70	76	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
771	LIB3602-068-Q1-K1-G4	1172977	BLASTX	638	2.00E-66	76	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
772	LIB3602-092-Q6-K6-E6	1172977	BLASTX	630	1.00E-65	73	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
773	LIB3602-003-Q1-K1-D12	1172977	BLASTX	573	5.00E-59	75	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
774	LIB3602-003-Q1-K1-G6	1172977	BLASTX	546	6.00E-56	75	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
775	LIB3602-057-Q6-K1-F7	1172977	BLASTX	439	6.00E-54	75	60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
776	LIB3602-056-Q6-K1-C4	1172977	BLASTX	498	3.00E-50	70	ribosomal protein L18 [Arabidopsis thaliana] 60S RIBOSOMAL PROTEIN L18 >gi 606970 gb AAA69928.1 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]
777	LIB3602-052-Q6-K1-F1	1350717	BLASTX	376	5.00E-36	67	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
778	LIB3602-011-Q6-K1-H2	1350717	BLASTX	339	1.00E-31	61	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
779	LIB3602-066-Q1-K6-H12	1350717	BLASTX	339	1.00E-31	61	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
780	LIB3602-066-Q1-K6-C7	1350717	BLASTX	339	1.00E-31	61	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
781	LIB3602-108-Q1-K1-A9	1350717	BLASTX	336	2.00E-31	60	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
782	LIB3602-106-Q1-K1-D4	1350717	BLASTX	336	3.00E-31	65	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
783	LIB3602-071-Q1-K1-H12	1350717	BLASTX	336	3.00E-31	65	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
784	LIB3602-056-Q6-K1-F12	1350717	BLASTX	331	8.00E-31	59	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
785	LIB3602-004-Q1-K1-C10	1350717	BLASTX	327	2.00E-30	65	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
786	LIB3602-049-Q6-K1-E8	1350717	BLASTX	276	1.00E-24	73	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
787	LIB3602-006-Q1-K1-G5	1350717	BLASTX	177	8.00E-13	68	60S RIBOSOMAL PROTEIN L30 >gi 422700 pir S34608 ribosomal protein L30, cytosolic - chicken >gi 402507 dbj BAA03394.1 (D14521) ribosomal protein L30 [Gallus gallus]
788	LIB3602-039-Q6-K1-G7	3717978	BLASTX	790	2.00E-84	80	(Y12431) 5S ribosomal protein [Mus musculus]
789	LIB3602-041-Q6-K1-F5	3717978	BLASTX	767	1.00E-81	80	(Y12431) 5S ribosomal protein [Mus musculus]
790	LIB3602-017-Q6-K1-C3	3717978	BLASTX	744	5.00E-79	81	(Y12431) 5S ribosomal protein [Mus musculus]
791	LIB3602-003-Q1-K1-G8	3717978	BLASTX	733	1.00E-77	79	(Y12431) 5S ribosomal protein [Mus musculus]
792	LIB3602-107-Q1-K1-A1	3717978	BLASTX	723	1.00E-76	78	(Y12431) 5S ribosomal protein [Mus musculus]
793	LIB3602-028-Q6-K1-E1	3717978	BLASTX	695	2.00E-73	79	(Y12431) 5S ribosomal protein [Mus musculus]
794	LIB3602-062-Q6-K1-C3	3717978	BLASTX	690	1.00E-72	78	(Y12431) 5S ribosomal protein [Mus musculus]
795	LIB3602-048-Q6-K1QA-C2	3717978	BLASTX	667	5.00E-70	77	(Y12431) 5S ribosomal protein [Mus musculus]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
796	LIB3602-045-Q6-K1-H5	3717978	BLASTX	585	2.00E-60	76	(Y12431) 5S ribosomal protein [Mus musculus]
797	LIB3602-108-Q1-K1-E8	3717978	BLASTX	418	4.00E-51	77	(Y12431) 5S ribosomal protein [Mus musculus]
798	LIB3602-051-Q6-K1-C12	3717978	BLASTX	366	8.00E-35	55	(Y12431) 5S ribosomal protein [Mus musculus]
799	LIB3602-093-Q6-K6-F4	1710551	BLASTX	187	3.00E-14	79	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
800	LIB3602-084-Q6-K1-F4	1710551	BLASTX	187	4.00E-14	79	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
801	LIB3602-062-Q6-K1-D1	1710551	BLASTX	167	8.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
802	LIB3602-012-Q6-K1-H11	1710551	BLASTX	167	8.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
803	LIB3602-040-Q6-K1-B8	1710551	BLASTX	167	8.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
804	LIB3602-014-Q6-K1-E2	1710551	BLASTX	167	8.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
805	LIB3602-022-Q6-K1-E5	1710551	BLASTX	167	8.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
806	LIB3602-032-Q6-K1-G2	1710551	BLASTX	167	8.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
807	LIB3602-102-Q1-K1-D12	1710551	BLASTX	167	9.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
808	LIB3602-045-Q6-K1-D8	1710551	BLASTX	167	9.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
809	LIB3602-055-Q6-K1-E3	1710551	BLASTX	167	9.00E-12	64	60S RIBOSOMAL PROTEIN L39 >gi 7440765 pir T03943 ribosomal protein L39 - maize >gi 1177369 emb CAA64728.1 (X95458) ribosomal protein L39 [Zea mays]
810	LIB3602-043-Q6-K1-F7	7433374	BLASTX	1032	1.00E-112	85	ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri >gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri]
811	LIB3602-043-Q6-K1-E3	7433374	BLASTX	928	1.00E-100	85	ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri >gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri]
812	LIB3602-014-Q6-K1-F3	7433374	BLASTX	928	1.00E-100	85	ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
813	LIB3602-026-Q6-K1-H1	7433374	BLASTX	526	3.00E-82	89	>gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri] ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri
814	LIB3602-048-Q6-K1QA-D4	7433374	BLASTX	759	8.00E-81	86	>gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri] ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri
815	LIB3602-057-Q6-K1-A11	7433374	BLASTX	709	9.00E-75	84	>gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri] ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri
816	LIB3602-108-Q1-K1-F6	7433374	BLASTX	571	9.00E-59	85	>gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri] ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri
817	LIB3602-073-Q1-K1-C12	7433374	BLASTX	565	5.00E-58	78	>gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri] ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri
818	LIB3602-018-Q6-K1-A4	7433374	BLASTX	420	5.00E-41	67	>gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri] ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri
819	LIB3602-019-Q6-K1-D5	7433374	BLASTX	294	2.00E-26	84	>gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri] ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri
820	LIB3602-109-Q1-K1-A3	7433374	BLASTX	166	1.00E-11	60	>gi 732532 gb AAB40978.1 (U22328) ferredoxin-NADP+ reductase [Volvox carteri] ferredoxin--NADP+ reductase (EC 1.18.1.2) precursor - Volvox carteri
821	LIB3602-062-Q6-K1-E10	6831665	BLASTX	705	2.00E-74	83	>gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
822	LIB3602-002-P1-K6-E10	6831665	BLASTX	651	4.00E-68	88	>gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
823	LIB3602-061-Q6-K1-C9	6831665	BLASTX	642	4.00E-67	87	>gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
824	LIB3602-120-Q1-K1-B8	6831665	BLASTX	512	4.00E-65	84	>gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
825	LIB3602-089-Q6-K6-G12	6831665	BLASTX	603	2.00E-62	87	>gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
826	LIB3602-120-Q1-K1-C11	6831665	BLASTX	422	9.00E-60	91	>gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
827	LIB3602-073-Q1-K1-F1	6831665	BLASTX	500	2.00E-50	86	>gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
828	LIB3602-093-Q6-K6-E4	6831665	BLASTX	453	1.00E-46	80	>gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
829	LIB3602-102-Q1-K1-E3	6831665	BLASTX	310	7.00E-46	92	40S RIBOSOMAL PROTEIN S5 >gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
830	LIB3602-042-Q6-K1-D12	6831665	BLASTX	458	1.00E-45	89	40S RIBOSOMAL PROTEIN S5 >gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
831	LIB3602-003-Q1-K1-D1	6831665	BLASTX	387	2.00E-37	61	40S RIBOSOMAL PROTEIN S5 >gi 3043428 emb CAA06491.1 (AJ005346) 40S ribosomal protein S5 [Cicer arietinum]
832	LIB3602-001-P1-K6-E10	4582468	BLASTX	827	9.00E-89	88	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
833	LIB3602-018-Q6-K1-E3	4582468	BLASTX	733	9.00E-78	84	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
834	LIB3602-044-Q6-K1-D7	4582468	BLASTX	725	7.00E-77	89	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
835	LIB3602-088-Q6-K6-G12	4582468	BLASTX	693	5.00E-73	84	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
836	LIB3602-118-Q1-K1-G12	4582468	BLASTX	551	2.00E-71	85	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
837	LIB3602-007-Q1-K1-F1	4582468	BLASTX	584	3.00E-62	81	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
838	LIB3602-038-Q6-K1-D4	4582468	BLASTX	484	1.00E-48	85	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
839	LIB3602-030-Q6-K1-G10	4582468	BLASTX	349	6.00E-33	80	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
840	LIB3602-019-Q6-K1-H6	4582468	BLASTX	341	5.00E-32	79	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
841	LIB3602-048-Q6-K1QA-F6	4582468	BLASTX	295	4.00E-27	82	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
842	LIB3602-015-Q6-K1-B4	4582468	BLASTX	210	1.00E-16	76	(AC007071) 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
843	LIB3602-015-Q6-K1-A2	5902596	BLASTX	443	1.00E-43	58	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
844	LIB3602-046-Q6-K1-A9	5902596	BLASTX	423	2.00E-41	57	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
845	LIB3602-027-Q6-K1-D2	5902596	BLASTX	344	4.00E-32	46	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
846	LIB3602-059-Q6-K1-A12	5902596	BLASTX	338	2.00E-31	56	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
847	LIB3602-007-Q1-K1-E5	5902596	BLASTX	336	2.00E-31	56	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
848	LIB3602-005-Q1-K1-D6	5902596	BLASTX	260	2.00E-22	42	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
849	LIB3602-057-Q6-K1-H11	5902596	BLASTX	211	1.00E-17	58	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
850	LIB3602-076-Q6-K6-E11	5902596	BLASTX	207	1.00E-16	67	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
851	LIB3602-095-Q6-K6-B3	5902596	BLASTX	206	4.00E-16	57	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
852	LIB3602-016-Q6-K1-E3	5902596	BLASTX	205	5.00E-16	67	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
853	LIB3602-018-Q6-K1-F11	5902596	BLASTX	194	1.00E-14	67	(AF110786) light harvesting complex a protein [Volvox carteri f. nagariensis]
854	LIB3602-072-Q1-K1-F5	6094476	BLASTX	559	3.00E-69	69	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
855	LIB3602-062-Q6-K1-H3	6094476	BLASTX	650	5.00E-68	68	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
856	LIB3602-059-Q6-K1-C7	6094476	BLASTX	622	9.00E-65	67	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
857	LIB3602-065-Q1-K6-B5	6094476	BLASTX	598	6.00E-62	66	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
858	LIB3602-103-Q1-K1-G3	6094476	BLASTX	585	2.00E-60	66	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
859	LIB3602-111-Q1-K1-D5	6094476	BLASTX	482	3.00E-59	72	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
860	LIB3602-044-Q6-K1-G8	6094476	BLASTX	553	1.00E-56	70	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
861	LIB3602-030-Q6-K1-G5	6094476	BLASTX	533	2.00E-54	65	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
862	LIB3602-054-Q6-K1-B11	6094476	BLASTX	448	2.00E-44	73	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
863	LIB3602-107-Q1-K1-G8	6094476	BLASTX	160	2.00E-10	73	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR >gi 7446894 pir T10474 thiamin biosynthesis protein thi1 - sweet orange >gi 2582665 emb CAB05370.1 (Z82983) thi [Citrus sinensis]
864	LIB3602-008-Q6-K1-H7	1173024	BLASTX	364	1.00E-34	66	60S RIBOSOMAL PROTEIN L31 >gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii >gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii]
865	LIB3602-071-Q1-K1-F2	1173024	BLASTX	360	4.00E-34	65	60S RIBOSOMAL PROTEIN L31 >gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii >gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii]
866	LIB3602-095-Q6-K6-B11	1173024	BLASTX	360	5.00E-34	65	60S RIBOSOMAL PROTEIN L31 >gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
867	LIB3602-087-Q6-K1-C1	1173024	BLASTX	358	8.00E-34	67	>gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii] 60S RIBOSOMAL PROTEIN L31
868	LIB3602-067-Q1-K1-C11	1173024	BLASTX	358	8.00E-34	67	>gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii >gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii] 60S RIBOSOMAL PROTEIN L31
869	LIB3602-105-Q1-K1-D2	1173024	BLASTX	342	7.00E-32	66	>gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii >gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii] 60S RIBOSOMAL PROTEIN L31
870	LIB3602-105-Q1-K1-C12	1173024	BLASTX	340	1.00E-31	62	>gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii >gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii] 60S RIBOSOMAL PROTEIN L31
871	LIB3602-020-Q6-K1-D9	1173024	BLASTX	269	1.00E-23	67	>gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii >gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii] 60S RIBOSOMAL PROTEIN L31
872	LIB3602-057-Q6-K1-E11	1173024	BLASTX	221	7.00E-18	51	>gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii >gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii] 60S RIBOSOMAL PROTEIN L31
873	LIB3602-022-Q6-K1-E6	1173024	BLASTX	177	9.00E-13	48	>gi 99421 pir S24989 ribosomal protein L31.e, cytosolic - Chlamydomonas reinhardtii >gi 18209 emb CAA47044.1 (X66413) ribosomal protein L31 [Chlamydomonas reinhardtii] 60S RIBOSOMAL PROTEIN L31
874	LIB3602-047-Q6-K1-A9	7269837	BLASTX	261	2.00E-22	84	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
875	LIB3602-043-Q6-K1-B4	7269837	BLASTX	261	2.00E-22	84	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
876	LIB3602-042-Q6-K1-F1	7269837	BLASTX	261	2.00E-22	84	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
877	LIB3602-032-Q6-K1-H4	7269837	BLASTX	261	2.00E-22	84	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
878	LIB3602-058-Q6-K1-B12	7269837	BLASTX	261	2.00E-22	84	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
879	LIB3602-019-Q6-K1-C8	7269837	BLASTX	258	3.00E-22	84	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
880	LIB3602-111-Q1-K1-G2	7269837	BLASTX	258	3.00E-22	83	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
881	LIB3602-109-Q1-K1-B11	7269837	BLASTX	252	2.00E-21	83	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
882	LIB3602-032-Q6-K1-A4	7269837	BLASTX	170	6.00E-12	78	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]
883	LIB3602-046-Q6-K1-F8	7269837	BLASTX	156	3.00E-10	65	(AL161574) RIBOSOMAL PROTEIN S30 homolog [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
884	LIB3602-104-Q1-K1-G6	133808	BLASTX	494	1.00E-49	77	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
885	LIB3602-113-Q1-K1-C8	133808	BLASTX	445	5.00E-44	81	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
886	LIB3602-065-Q1-K6-A4	133808	BLASTX	434	9.00E-43	83	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
887	LIB3602-120-Q1-K1-C8	133808	BLASTX	270	6.00E-41	87	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
888	LIB3602-052-Q6-K1-G8	133808	BLASTX	354	9.00E-39	87	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
889	LIB3602-027-Q6-K1-F8	133808	BLASTX	365	9.00E-35	86	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
890	LIB3602-042-Q6-K1-A8	133808	BLASTX	354	2.00E-33	87	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
891	LIB3602-088-Q6-K6-E2	133808	BLASTX	240	2.00E-31	80	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
892	LIB3602-076-Q6-K6-A9	133808	BLASTX	265	7.00E-23	87	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
893	LIB3602-095-Q6-K6-A2	133808	BLASTX	256	3.00E-22	90	40S RIBOSOMAL PROTEIN S16 >gi 70921 pir R3YL16 ribosomal protein S16, cytosolic - large-leaved lupine >gi 19512 emb CAA36068.1 (X51766) rps16 gene product (AA 1-145) [Lupinus polyphyllus]
894	LIB3602-061-Q6-K1-A11	130263	BLASTX	407	1.00E-39	76	PLASTOCYANIN >gi 65845 pir CUKLFC plastocyanin - Chlorella fusca
895	LIB3602-113-Q1-K1-E2	130263	BLASTX	407	2.00E-39	76	PLASTOCYANIN >gi 65845 pir CUKLFC plastocyanin - Chlorella fusca
896	LIB3602-035-Q1-K1-A9	130263	BLASTX	407	2.00E-39	76	PLASTOCYANIN >gi 65845 pir CUKLFC plastocyanin - Chlorella fusca
897	LIB3602-054-Q6-K1-D4	130263	BLASTX	401	6.00E-39	75	PLASTOCYANIN >gi 65845 pir CUKLFC plastocyanin - Chlorella fusca

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
898	LIB3602-092-Q6-K6-G3	130263	BLASTX	399	2.00E-38	75	PLASTOCYANIN >gi 65845 pir CUKLCF plastocyanin - Chlorella fusca
899	LIB3602-089-Q6-K6-A3	130263	BLASTX	397	2.00E-38	75	PLASTOCYANIN >gi 65845 pir CUKLCF plastocyanin - Chlorella fusca
900	LIB3602-073-Q1-K1-A5	130263	BLASTX	323	4.00E-34	78	PLASTOCYANIN >gi 65845 pir CUKLCF plastocyanin - Chlorella fusca
901	LIB3602-087-Q6-K1-G9	130263	BLASTX	232	5.00E-32	68	PLASTOCYANIN >gi 65845 pir CUKLCF plastocyanin - Chlorella fusca
902	LIB3602-034-Q6-K1-A9	130263	BLASTX	302	2.00E-27	76	PLASTOCYANIN >gi 65845 pir CUKLCF plastocyanin - Chlorella fusca
903	LIB3602-062-Q6-K1-C6	130263	BLASTX	232	3.00E-19	71	PLASTOCYANIN >gi 65845 pir CUKLCF plastocyanin - Chlorella fusca
904	LIB3602-078-Q6-K6-E10	7441093	BLASTX	500	2.00E-50	72	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]
							>gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
905	LIB3602-053-Q6-K1-F1	7441093	BLASTX	500	2.00E-50	72	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]
							>gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
906	LIB3602-066-Q1-K6-G5	7441093	BLASTX	492	2.00E-49	72	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]
							>gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
907	LIB3602-077-Q6-K6-G8	7441093	BLASTX	373	5.00E-45	73	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]
							>gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
908	LIB3602-040-Q6-K1-A12	7441093	BLASTX	452	6.00E-45	77	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]
							>gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
909	LIB3602-003-Q1-K1-C10	7441093	BLASTX	356	9.00E-34	73	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]
							>gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
910	LIB3602-065-Q1-K6-D6	7441093	BLASTX	278	3.00E-33	70	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
911	LIB3602-003-Q1-K1-C11	7441093	BLASTX	283	3.00E-25	67	>gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana] ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana] >gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
912	LIB3602-032-Q6-K1-E2	7441093	BLASTX	201	1.00E-15	75	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana] >gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
913	LIB3602-043-Q6-K1-A12	7441093	BLASTX	199	1.00E-15	76	ribosomal protein L32, cytosolic - Arabidopsis thaliana >gi 5816996 emb CAB53651.1 (AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana] >gi 7268562 emb CAB78812.1 (AL161547) ribosomal protein L32-like protein [Arabidopsis thaliana]
914	LIB3602-077-Q6-K6-E8	3914685	BLASTX	563	9.00E-58	69	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
915	LIB3602-058-Q6-K1-A8	3914685	BLASTX	556	5.00E-57	71	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
916	LIB3602-073-Q1-K1-G2	3914685	BLASTX	556	6.00E-57	71	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
917	LIB3602-028-Q6-K1-E6	3914685	BLASTX	545	1.00E-55	72	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
918	LIB3602-102-Q1-K1-G3	3914685	BLASTX	542	2.00E-55	72	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
919	LIB3602-041-Q6-K1-E2	3914685	BLASTX	542	2.00E-55	72	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
920	LIB3602-079-Q6-K6-F1	3914685	BLASTX	542	3.00E-55	72	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
921	LIB3602-088-Q6-K6-C3	3914685	BLASTX	495	3.00E-51	70	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
922	LIB3602-100-Q1-K1-H8	3914685	BLASTX	382	5.00E-50	74	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 -

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
923	LIB3602-014-Q6-K1-C5	3914685	BLASTX	450	1.00E-44	71	maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
924	LIB3602-017-Q6-K1-B1	6984142	BLASTX	315	8.00E-29	82	60S RIBOSOMAL PROTEIN L17 >gi 7440981 pir T01410 ribosomal protein L17 - maize >gi 2668748 gb AAB88619.1 (AF034948) ribosomal protein L17 [Zea mays]
925	LIB3602-102-Q1-K1-C10	6984142	BLASTX	311	2.00E-28	83	(AF227626) 40S ribosomal protein S11 [Euphorbia esula]
926	LIB3602-078-Q6-K6-H10	6984142	BLASTX	309	4.00E-28	75	(AF227626) 40S ribosomal protein S11 [Euphorbia esula]
927	LIB3602-070-Q1-K1-A8	6984142	BLASTX	306	9.00E-28	83	(AF227626) 40S ribosomal protein S11 [Euphorbia esula]
928	LIB3602-066-Q1-K6-D11	6984142	BLASTX	306	9.00E-28	83	(AF227626) 40S ribosomal protein S11 [Euphorbia esula]
929	LIB3602-100-Q1-K1-H4	6984142	BLASTX	202	4.00E-23	81	(AF227626) 40S ribosomal protein S11 [Euphorbia esula]
930	LIB3602-067-Q1-K1-B2	6984142	BLASTX	203	5.00E-23	82	(AF227626) 40S ribosomal protein S11 [Euphorbia esula]
931	LIB3602-064-Q1-K6-G6	6984142	BLASTX	251	2.00E-21	77	(AF227626) 40S ribosomal protein S11 [Euphorbia esula]
932	LIB3602-079-Q6-K6-D11	6984142	BLASTX	211	3.00E-17	77	(AF227626) 40S ribosomal protein S11 [Euphorbia esula]
933	LIB3602-053-Q6-K1-D9	121026	BLASTX	942	1.00E-102	88	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta subunit [Ch
934	LIB3602-105-Q1-K1-B4	121026	BLASTX	845	9.00E-95	91	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta subunit [Ch
935	LIB3602-072-Q1-K1-E1	121026	BLASTX	792	1.00E-84	87	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta subunit [Ch
936	LIB3602-053-Q6-K1-F7	121026	BLASTX	700	6.00E-74	86	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta subunit [Ch
937	LIB3602-043-Q6-K1-D1	121026	BLASTX	570	1.00E-58	88	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
938	LIB3602-059-Q6-K1-G12	121026	BLASTX	566	4.00E-58	88	subunit [Ch GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta subunit [Ch
939	LIB3602-101-Q1-K1-E1	121026	BLASTX	244	2.00E-20	83	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta subunit [Ch
940	LIB3602-071-Q1-K1-A1	121026	BLASTX	214	6.00E-17	82	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta subunit [Ch
941	LIB3602-106-Q1-K1-C5	121026	BLASTX	160	1.00E-12	85	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN >gi 99395 pir S11904 GTP-binding regulatory protein beta chain homolog - Chlamydomonas reinhardtii >gi 18145 emb CAA37638.1 (X53574) putative protein has homology to G protein beta subunit [Ch
942	LIB3602-044-Q6-K1-F8	4506697	BLASTX	475	1.00E-47	78	ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20, cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote
943	LIB3602-085-Q6-K1-B1	4506697	BLASTX	475	1.00E-47	78	ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20, cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote
944	LIB3602-042-Q6-K1-D2	4506697	BLASTX	475	2.00E-47	78	ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20, cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote
945	LIB3602-027-Q6-K1-G1	4506697	BLASTX	475	2.00E-47	78	ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20,

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
946	LIB3602-007-Q1-K1-A7	4506697	BLASTX	472	3.00E-47	84	cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20, cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote
947	LIB3602-022-Q6-K1-C2	4506697	BLASTX	451	7.00E-45	76	ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20, cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote
948	LIB3602-003-Q1-K1-F12	4506697	BLASTX	450	1.00E-44	74	ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20, cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote
949	LIB3602-108-Q1-K1-G4	4506697	BLASTX	311	3.00E-42	82	ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20, cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote
950	LIB3602-007-Q1-K1-C3	4506697	BLASTX	428	5.00E-42	73	ribosomal protein S20 >gi 133875 sp P17075 RS20_HUMAN 40S RIBOSOMAL PROTEIN S20 >gi 70925 pir R3RT20 ribosomal protein S20, cytosolic - rat >gi 423075 pir S33710 ribosomal protein S20, cytosolic - human >gi 57720 emb CAA35917.1 (X51537) ribosomal prote
951	LIB3602-078-Q6-K6-F6	6521012	BLASTX	634	4.00E-66	82	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]
952	LIB3602-089-Q6-K6-C6	6521012	BLASTX	631	9.00E-66	82	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]
953	LIB3602-083-Q6-K6-H6	6521012	BLASTX	538	8.00E-61	78	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]
954	LIB3602-010-Q6-K1-A4	6521012	BLASTX	540	4.00E-55	82	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]
955	LIB3602-028-Q6-K1-F9	6521012	BLASTX	538	7.00E-55	82	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]
956	LIB3602-010-Q6-K1-A5	6521012	BLASTX	511	1.00E-51	84	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]
957	LIB3602-105-Q1-K1-G3	6521012	BLASTX	483	2.00E-48	86	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
958	LIB3602-118-Q1-K1-A1	6521012	BLASTX	311	8.00E-43	83	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]
959	LIB3602-023-Q6-K1-B5	6521012	BLASTX	218	2.00E-17	71	(AB031739) cytoplasmic ribosomal protein S13 [Arabidopsis thaliana]
960	LIB3602-078-Q6-K6-H9	1351014	BLASTX	655	1.00E-68	68	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
961	LIB3602-039-Q6-K1-A12	1351014	BLASTX	572	7.00E-59	65	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
962	LIB3602-010-Q6-K1-D8	1351014	BLASTX	518	1.00E-52	66	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
963	LIB3602-003-Q1-K1-E12	1351014	BLASTX	515	3.00E-52	64	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
964	LIB3602-083-Q6-K6-H5	1351014	BLASTX	509	2.00E-51	63	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
965	LIB3602-109-Q1-K1-H5	1351014	BLASTX	334	1.00E-44	61	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
966	LIB3602-014-Q6-K1-C9	1351014	BLASTX	257	5.00E-22	55	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
967	LIB3602-037-Q6-K1-B1	1351014	BLASTX	242	8.00E-21	68	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
968	LIB3602-011-Q6-K1-D7	1351014	BLASTX	225	3.00E-18	69	40S RIBOSOMAL PROTEIN S8 >gi 7440236 pir T04082 probable ribosomal protein S8 - rice >gi 968902 dbj BAA07207.1 (D38010) ribosomal protein S8 [Oryza sativa]
969	LIB3602-095-Q6-K6-F2	6174958	BLASTX	778	6.00E-83	72	60S RIBOSOMAL PROTEIN L7 >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana >gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana]
970	LIB3602-089-Q6-K6-F2	6174958	BLASTX	753	5.00E-80	71	60S RIBOSOMAL PROTEIN L7 >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana >gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana]
971	LIB3602-076-Q6-K6-F4	6174958	BLASTX	677	4.00E-71	67	60S RIBOSOMAL PROTEIN L7 >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana >gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana]
972	LIB3602-044-Q6-K1-G11	6174958	BLASTX	633	4.00E-66	75	60S RIBOSOMAL PROTEIN L7 >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
973	LIB3602-006-Q1-K1-C1	6174958	BLASTX	632	7.00E-66	67	>gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana] >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana
974	LIB3602-043-Q6-K1-D11	6174958	BLASTX	622	1.00E-64	74	>gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana] >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana
975	LIB3602-027-Q6-K1-E10	6174958	BLASTX	609	3.00E-63	75	>gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana] >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana
976	LIB3602-060-Q6-K1-H2	6174958	BLASTX	598	6.00E-62	75	>gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana] >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana
977	LIB3602-054-Q6-K1-F11	6174958	BLASTX	206	5.00E-16	33	>gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana] >gi 7440720 pir T00692 ribosomal protein L7, cytosolic - Arabidopsis thaliana
978	LIB3602-046-Q6-K1-A11	1173187	BLASTX	677	3.00E-71	90	>gi 3212879 gb AAC23430.1 (AC004005) 60S ribosomal protein L7 [Arabidopsis thaliana] >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry
979	LIB3602-030-Q6-K1-C8	1173187	BLASTX	677	3.00E-71	90	>gi 643074 gb AAA79921.1 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa] >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry
980	LIB3602-039-Q6-K1-E1	1173187	BLASTX	677	4.00E-71	90	>gi 643074 gb AAA79921.1 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa] >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry
981	LIB3602-067-Q1-K1-F6	1173187	BLASTX	674	9.00E-71	89	>gi 643074 gb AAA79921.1 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa] >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry
982	LIB3602-100-Q1-K1-F9	1173187	BLASTX	488	7.00E-66	94	>gi 643074 gb AAA79921.1 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa] >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry
983	LIB3602-037-Q6-K1-B2	1173187	BLASTX	582	3.00E-60	90	>gi 643074 gb AAA79921.1 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa] >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
984	LIB3602-022-Q6-K1-C8	1173187	BLASTX	582	4.00E-60	90	40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi 643074 gb AAA79921.1 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]
985	LIB3602-046-Q6-K1-A12	1173187	BLASTX	536	7.00E-55	87	40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi 643074 gb AAA79921.1 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]
986	LIB3602-021-Q6-K1-D3	1173187	BLASTX	344	1.00E-32	87	40S RIBOSOMAL PROTEIN S23 (S12) >gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi 643074 gb AAA79921.1 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]
987	LIB3602-068-Q1-K1-D1	6671950	BLASTX	439	2.00E-43	90	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
988	LIB3602-081-Q6-K6-G1	6671950	BLASTX	405	2.00E-39	96	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
989	LIB3602-086-Q6-K1-E5	6671950	BLASTX	405	2.00E-39	96	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
990	LIB3602-023-Q6-K1-G12	6671950	BLASTX	376	5.00E-36	96	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
991	LIB3602-117-Q1-K1-B8	6671950	BLASTX	190	1.00E-30	97	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
992	LIB3602-055-Q6-K1-C8	6671950	BLASTX	318	3.00E-29	91	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
993	LIB3602-057-Q6-K1-E12	6671950	BLASTX	186	2.00E-28	90	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
994	LIB3602-026-Q6-K1-F5	6671950	BLASTX	240	1.00E-21	84	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
995	LIB3602-007-Q1-K1-B2	6671950	BLASTX	209	5.00E-17	89	(AC016795) putative 40S ribosomal protein S5 [Arabidopsis thaliana]
996	LIB3602-036-Q6-K1-A8	99487	BLASTX	449	2.00E-44	60	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]
997	LIB3602-068-Q1-K1-B5	99487	BLASTX	398	2.00E-38	60	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]
998	LIB3602-052-Q6-K1-G12	99487	BLASTX	381	1.00E-36	58	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]
999	LIB3602-048-Q6-K1QA-H11	99487	BLASTX	348	8.00E-33	61	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]
1000	LIB3602-020-Q6-K1-F5	99487	BLASTX	343	4.00E-32	61	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]
1001	LIB3602-112-Q1-K1-F10	99487	BLASTX	329	3.00E-30	62	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1002	LIB3602-089-Q6-K6-F10	99487	BLASTX	320	3.00E-29	60	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]
1003	LIB3602-021-Q6-K1-H2	99487	BLASTX	157	1.00E-10	58	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]
1004	LIB3602-118-Q1-K1-C11	99487	BLASTX	157	3.00E-10	58	chlorophyll a/b-binding protein (clone pINEab 43) - Scotch pine >gi 20794 emb CAA41407.1 (X58517) Type III chlorophyll a /b-binding protein [Pinus sylvestris]
1005	LIB3602-030-Q6-K1-B7	3953473	BLASTX	271	1.00E-23	54	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1006	LIB3602-083-Q6-K6-C9	3953473	BLASTX	271	1.00E-23	54	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1007	LIB3602-054-Q6-K1-G2	3953473	BLASTX	271	1.00E-23	54	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1008	LIB3602-109-Q1-K1-C9	3953473	BLASTX	265	7.00E-23	59	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1009	LIB3602-053-Q6-K1-D12	3953473	BLASTX	264	1.00E-22	53	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1010	LIB3602-079-Q6-K6-A1	3953473	BLASTX	240	4.00E-20	57	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1011	LIB3602-067-Q1-K1-B12	3953473	BLASTX	216	2.00E-17	60	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1012	LIB3602-087-Q6-K1-E2	3953473	BLASTX	216	2.00E-17	60	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1013	LIB3602-056-Q6-K1-F2	3953473	BLASTX	145	2.00E-13	57	(AC002328) F22O2.18 [Arabidopsis thaliana] >gi 5734520 emb CAB52748.1 (AJ245630) photosystem I subunit V precursor [Arabidopsis thaliana]
1014	LIB3602-054-Q6-K1-F10	131395	BLASTX	383	8.00E-37	59	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3 precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1015	LIB3602-071-Q1-K1-G3	131395	BLASTX	260	7.00E-30	55	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1016	LIB3602-102-Q1-K1-F3	131395	BLASTX	297	8.00E-27	57	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3 precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1017	LIB3602-016-Q6-K1-C7	131395	BLASTX	292	4.00E-26	57	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3 precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1018	LIB3602-073-Q1-K1-H1	131395	BLASTX	260	3.00E-22	55	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3 precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1019	LIB3602-109-Q1-K1-D7	131395	BLASTX	148	7.00E-16	60	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3 precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1020	LIB3602-119-Q1-K1-E1	131395	BLASTX	199	2.00E-15	54	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3 precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1021	LIB3602-092-Q6-K6-G4	131395	BLASTX	199	5.00E-15	54	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3 precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1022	LIB3602-054-Q6-K1-F5	131395	BLASTX	145	6.00E-09	48	OXYGEN-EVOLVING ENHANCER PROTEIN 3 PRECURSOR (OEE3) >gi 81254 pir S05509 photosystem II oxygen-evolving complex protein 3 precursor - Chlamydomonas reinhardtii >gi 18164 emb CAA32061.1 (X13832) OEE3 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1023	LIB3602-047-Q6-K1-F1	7413571	BLASTX	505	4.00E-51	94	(AL162973) putative protein [Arabidopsis thaliana]
1024	LIB3602-084-Q6-K1-B10	7413571	BLASTX	455	1.00E-46	92	(AL162973) putative protein [Arabidopsis thaliana]
1025	LIB3602-008-Q6-K1-C6	7413571	BLASTX	422	2.00E-41	92	(AL162973) putative protein [Arabidopsis thaliana]
1026	LIB3602-083-Q6-K6-A7	7413571	BLASTX	413	3.00E-40	94	(AL162973) putative protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1027	LIB3602-008-Q6-K1-C3	7413571	BLASTX	411	5.00E-40	90	(AL162973) putative protein [Arabidopsis thaliana]
1028	LIB3602-091-Q6-K6-A3	7413571	BLASTX	299	8.00E-27	81	(AL162973) putative protein [Arabidopsis thaliana]
1029	LIB3602-095-Q6-K6-A3	7413571	BLASTX	298	1.00E-26	91	(AL162973) putative protein [Arabidopsis thaliana]
1030	LIB3602-094-Q6-K6-A3	7413571	BLASTX	213	5.00E-21	88	(AL162973) putative protein [Arabidopsis thaliana]
1031	LIB3602-039-Q6-K1-E2	7413571	BLASTX	222	4.00E-18	48	(AL162973) putative protein [Arabidopsis thaliana]
1032	LIB3602-113-Q1-K1-G7	5821436	BLASTX	721	3.00E-76	69	(AB031546) chloroplast w6 desaturase [Chlamydomonas sp. W80]
1033	LIB3602-015-Q6-K1-H9	5821436	BLASTX	689	1.00E-72	65	(AB031546) chloroplast w6 desaturase [Chlamydomonas sp. W80]
1034	LIB3602-108-Q1-K1-C5	5821436	BLASTX	616	4.00E-64	70	(AB031546) chloroplast w6 desaturase [Chlamydomonas sp. W80]
1035	LIB3602-120-Q1-K1-G7	5821436	BLASTX	601	2.00E-62	72	(AB031546) chloroplast w6 desaturase [Chlamydomonas sp. W80]
1036	LIB3602-113-Q1-K1-C2	5821436	BLASTX	560	2.00E-57	66	(AB031546) chloroplast w6 desaturase [Chlamydomonas sp. W80]
1037	LIB3602-120-Q1-K1-C2	5821436	BLASTX	466	1.00E-46	66	(AB031546) chloroplast w6 desaturase [Chlamydomonas sp. W80]
1038	LIB3602-092-Q6-K6-D2	5821436	BLASTX	424	2.00E-41	74	(AB031546) chloroplast w6 desaturase [Chlamydomonas sp. W80]
1039	LIB3602-021-Q6-K1-E5	5821436	BLASTX	314	4.00E-29	69	(AB031546) chloroplast w6 desaturase [Chlamydomonas sp. W80]
1040	LIB3602-104-Q1-K1-D3	1173209	BLASTX	554	1.00E-56	78	40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal protein S16 protein - upland cotton >gi 439654 emb CAA53567.1 (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
1041	LIB3602-051-Q6-K1-E2	1173209	BLASTX	538	6.00E-55	74	40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal protein S16 protein - upland cotton >gi 439654 emb CAA53567.1 (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
1042	LIB3602-035-Q1-K1-B1	1173209	BLASTX	530	8.00E-54	75	40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal protein S16 protein - upland cotton >gi 439654 emb CAA53567.1 (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
1043	LIB3602-063-Q1-K6-C12	1173209	BLASTX	530	8.00E-54	75	40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal protein S16 protein - upland cotton >gi 439654 emb CAA53567.1 (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
1044	LIB3602-101-Q1-K1-H1	1173209	BLASTX	429	5.00E-53	82	40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal protein S16 protein - upland cotton >gi 439654 emb CAA53567.1 (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
1045	LIB3602-022-Q6-K1-H6	1173209	BLASTX	515	2.00E-52	77	40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal protein S16 protein - upland cotton >gi 439654 emb CAA53567.1 (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
1046	LIB3602-107-Q1-K1-D4	1173209	BLASTX	275	9.00E-50	66	40S RIBOSOMAL PROTEIN S16 >gi 541835 pir S41193 ribosomal protein S16 protein - upland cotton >gi 439654 emb CAA53567.1 (X75954) RS16 protein, 40S subunit [Gossypium hirsutum]
1047	LIB3602-066-Q1-K6-D10	1173209	BLASTX	281	7.00E-25	65	40S RIBOSOMAL PROTEIN S16

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							>gi 541835 pir S41193 ribosomal protein S16 protein - upland cotton
							>gi 439654 emb CAA53567.1 (X75954) RS16 protein, 40S subunit [<i>Gossypium hirsutum</i>]
1048	LIB3602-093-Q6-K6-C12	5932542	BLASTX	473	2.00E-47	77	(AC009465) putative ribosomal protein s19 or s24 [<i>Arabidopsis thaliana</i>]
1049	LIB3602-012-Q6-K1-G9	5932542	BLASTX	469	7.00E-47	78	(AC009465) putative ribosomal protein s19 or s24 [<i>Arabidopsis thaliana</i>]
1050	LIB3602-045-Q6-K1-H11	5932542	BLASTX	469	7.00E-47	78	(AC009465) putative ribosomal protein s19 or s24 [<i>Arabidopsis thaliana</i>]
1051	LIB3602-060-Q6-K1-A8	5932542	BLASTX	466	2.00E-46	77	(AC009465) putative ribosomal protein s19 or s24 [<i>Arabidopsis thaliana</i>]
1052	LIB3602-087-Q6-K1-F5	5932542	BLASTX	441	1.00E-43	76	(AC009465) putative ribosomal protein s19 or s24 [<i>Arabidopsis thaliana</i>]
1053	LIB3602-025-Q6-K1-D8	5932542	BLASTX	341	4.00E-32	75	(AC009465) putative ribosomal protein s19 or s24 [<i>Arabidopsis thaliana</i>]
1054	LIB3602-062-Q6-K1-H12	5932542	BLASTX	333	4.00E-31	74	(AC009465) putative ribosomal protein s19 or s24 [<i>Arabidopsis thaliana</i>]
1055	LIB3602-119-Q1-K1-C12	5932542	BLASTX	290	2.00E-26	80	(AC009465) putative ribosomal protein s19 or s24 [<i>Arabidopsis thaliana</i>]
1056	LIB3602-107-Q1-K1-F9	7428635	BLASTX	261	2.00E-22	42	cyanoglobin - <i>Synechocystis</i> sp. (strain PCC 6803)
							>gi 1653074 dbj BAA17991.1 (D90910)
							cyanoglobin [<i>Synechocystis</i> sp.]
1057	LIB3602-001-P1-K6-A10	7428635	BLASTX	261	2.00E-22	42	cyanoglobin - <i>Synechocystis</i> sp. (strain PCC 6803)
							>gi 1653074 dbj BAA17991.1 (D90910)
							cyanoglobin [<i>Synechocystis</i> sp.]
1058	LIB3602-089-Q6-K6-E2	7428635	BLASTX	259	4.00E-22	45	cyanoglobin - <i>Synechocystis</i> sp. (strain PCC 6803)
							>gi 1653074 dbj BAA17991.1 (D90910)
							cyanoglobin [<i>Synechocystis</i> sp.]
1059	LIB3602-056-Q6-K1-A1	7428635	BLASTX	194	1.00E-14	42	cyanoglobin - <i>Synechocystis</i> sp. (strain PCC 6803)
							>gi 1653074 dbj BAA17991.1 (D90910)
							cyanoglobin [<i>Synechocystis</i> sp.]
1060	LIB3602-023-Q6-K1-B2	7428635	BLASTX	183	3.00E-13	41	cyanoglobin - <i>Synechocystis</i> sp. (strain PCC 6803)
							>gi 1653074 dbj BAA17991.1 (D90910)
							cyanoglobin [<i>Synechocystis</i> sp.]
1061	LIB3602-050-Q6-K1-F8	7428635	BLASTX	171	6.00E-12	45	cyanoglobin - <i>Synechocystis</i> sp. (strain PCC 6803)
							>gi 1653074 dbj BAA17991.1 (D90910)
							cyanoglobin [<i>Synechocystis</i> sp.]
1062	LIB3602-100-Q1-K1-G12	7428635	BLASTX	166	2.00E-11	42	cyanoglobin - <i>Synechocystis</i> sp. (strain PCC 6803)
							>gi 1653074 dbj BAA17991.1 (D90910)
							cyanoglobin [<i>Synechocystis</i> sp.]
1063	LIB3602-053-Q6-K1-H5	7428635	BLASTX	151	1.00E-09	43	cyanoglobin - <i>Synechocystis</i> sp. (strain PCC 6803)
							>gi 1653074 dbj BAA17991.1 (D90910)
							cyanoglobin [<i>Synechocystis</i> sp.]
1064	LIB3602-078-Q6-K6-G8	2407314	BLASTX	691	9.00E-73	74	(AF017998) chlorophyll a/b binding protein [<i>Tetraselmis</i> sp. RG-15]
1065	LIB3602-088-Q6-K6-H5	2407314	BLASTX	524	2.00E-67	70	(AF017998) chlorophyll a/b binding protein [<i>Tetraselmis</i> sp. RG-15]
1066	LIB3602-023-Q6-K1-D5	2407314	BLASTX	591	4.00E-61	72	(AF017998) chlorophyll a/b binding protein [<i>Tetraselmis</i> sp. RG-15]
1067	LIB3602-049-Q6-K1-F1	2407314	BLASTX	544	1.00E-55	76	(AF017998) chlorophyll a/b binding protein [<i>Tetraselmis</i> sp. RG-15]
1068	LIB3602-032-Q6-K1-H5	2407314	BLASTX	539	4.00E-55	76	(AF017998) chlorophyll a/b binding protein [<i>Tetraselmis</i> sp. RG-15]
1069	LIB3602-056-Q6-K1-G1	2407314	BLASTX	524	2.00E-53	76	(AF017998) chlorophyll a/b binding protein [<i>Tetraselmis</i> sp. RG-15]
1070	LIB3602-052-Q6-K1-G5	2407314	BLASTX	479	4.00E-48	78	(AF017998) chlorophyll a/b binding protein [<i>Tetraselmis</i> sp. RG-15]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1071	LIB3602-043-Q6-K1-A1	2407314	BLASTX	349	5.00E-33	75	(AF017998) chlorophyll a/b binding protein [Tetraselmis sp. RG-15]
1072	LIB3602-092-Q6-K6-F7	131389	BLASTX	724	1.00E-76	69	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) >gi 81253 pir S00413 photosystem II oxygen-evolving complex protein 2 precursor - Chlamydomonas reinhardtii >gi 167428 gb AAA33088.1 (M15187) oxygen-evolving enhancer protein 2 [Chlamydomonas reinhardt]
1073	LIB3602-015-Q6-K1-H5	131389	BLASTX	694	4.00E-73	69	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) >gi 81253 pir S00413 photosystem II oxygen-evolving complex protein 2 precursor - Chlamydomonas reinhardtii >gi 167428 gb AAA33088.1 (M15187) oxygen-evolving enhancer protein 2 [Chlamydomonas reinhardt]
1074	LIB3602-081-Q6-K6-D8	131389	BLASTX	568	2.00E-58	70	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) >gi 81253 pir S00413 photosystem II oxygen-evolving complex protein 2 precursor - Chlamydomonas reinhardtii >gi 167428 gb AAA33088.1 (M15187) oxygen-evolving enhancer protein 2 [Chlamydomonas reinhardt]
1075	LIB3602-009-Q6-K1-H12	131389	BLASTX	391	8.00E-38	57	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) >gi 81253 pir S00413 photosystem II oxygen-evolving complex protein 2 precursor - Chlamydomonas reinhardtii >gi 167428 gb AAA33088.1 (M15187) oxygen-evolving enhancer protein 2 [Chlamydomonas reinhardt]
1076	LIB3602-017-Q6-K1-C9	131389	BLASTX	374	1.00E-35	77	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) >gi 81253 pir S00413 photosystem II oxygen-evolving complex protein 2 precursor - Chlamydomonas reinhardtii >gi 167428 gb AAA33088.1 (M15187) oxygen-evolving enhancer protein 2 [Chlamydomonas reinhardt]
1077	LIB3602-047-Q6-K1-E7	131389	BLASTX	356	1.00E-33	58	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) >gi 81253 pir S00413 photosystem II oxygen-evolving complex protein 2 precursor - Chlamydomonas reinhardtii >gi 167428 gb AAA33088.1 (M15187) oxygen-evolving enhancer protein 2 [Chlamydomonas reinhardt]
1078	LIB3602-040-Q6-K1-D4	131389	BLASTX	323	9.00E-30	59	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) >gi 81253 pir S00413 photosystem II oxygen-evolving complex protein 2 precursor - Chlamydomonas reinhardtii >gi 167428 gb AAA33088.1 (M15187) oxygen-evolving enhancer protein 2 [Chlamydomonas reinhardt]
1079	LIB3602-037-Q6-K1-C4	131389	BLASTX	277	2.00E-24	80	OXYGEN-EVOLVING ENHANCER PROTEIN 2 PRECURSOR (OEE2) >gi 81253 pir S00413 photosystem II oxygen-evolving complex protein 2 precursor - Chlamydomonas reinhardtii >gi 167428 gb AAA33088.1 (M15187) oxygen-evolving enhancer protein 2 [Chlamydomonas reinhardt]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1080	LIB3602-104-Q1-K1-B9	6723436	BLASTX	439	3.00E-43	64	(AL132965) 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]
1081	LIB3602-088-Q6-K6-D6	6723436	BLASTX	439	3.00E-43	64	(AL132965) 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]
1082	LIB3602-048-Q6-K1QA-C7	6723436	BLASTX	439	3.00E-43	64	(AL132965) 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]
1083	LIB3602-011-Q6-K1-E12	6723436	BLASTX	431	2.00E-42	63	(AL132965) 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]
1084	LIB3602-017-Q6-K1-A2	6723436	BLASTX	268	2.00E-23	59	(AL132965) 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]
1085	LIB3602-068-Q1-K1-D7	6723436	BLASTX	222	9.00E-18	89	(AL132965) 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]
1086	LIB3602-078-Q6-K6-B9	6723436	BLASTX	197	3.00E-15	54	(AL132965) 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]
1087	LIB3602-066-Q1-K6-B9	6723436	BLASTX	173	6.00E-13	88	(AL132965) 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]
1088	LIB3602-029-Q6-K1-E7	7488205	BLASTX	205	2.00E-20	43	probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana >gi 5051790 emb CAB45083.1 (AL078637) putative protein kinase [Arabidopsis thaliana] >gi 7269298 emb CAB79358.1 (AL161561) putative protein kinase [Arabidops
1089	LIB3602-034-Q6-K1-B4	7488205	BLASTX	187	8.00E-14	40	probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana >gi 5051790 emb CAB45083.1 (AL078637) putative protein kinase [Arabidopsis thaliana] >gi 7269298 emb CAB79358.1 (AL161561) putative protein kinase [Arabidops
1090	LIB3602-010-Q6-K1-H10	7488205	BLASTX	187	1.00E-13	38	probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana >gi 5051790 emb CAB45083.1 (AL078637) putative protein kinase [Arabidopsis thaliana] >gi 7269298 emb CAB79358.1 (AL161561) putative protein kinase [Arabidops
1091	LIB3602-035-Q1-K1-B4	7488205	BLASTX	181	5.00E-13	40	probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana >gi 5051790 emb CAB45083.1 (AL078637) putative protein kinase [Arabidopsis thaliana] >gi 7269298 emb CAB79358.1 (AL161561) putative protein kinase [Arabidops
1092	LIB3602-019-Q6-K1-C7	7488205	BLASTX	181	5.00E-13	28	probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana >gi 5051790 emb CAB45083.1 (AL078637) putative protein kinase [Arabidopsis thaliana] >gi 7269298 emb CAB79358.1 (AL161561) putative protein kinase [Arabidops
1093	LIB3602-073-Q1-K1-B12	7488205	BLASTX	180	6.00E-13	39	probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana >gi 5051790 emb CAB45083.1 (AL078637) putative protein kinase [Arabidopsis thaliana] >gi 7269298 emb CAB79358.1 (AL161561) putative protein kinase [Arabidops
1094	LIB3602-025-Q6-K1-G5	7488205	BLASTX	171	7.00E-12	31	probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis thaliana >gi 5051790 emb CAB45083.1 (AL078637) putative protein kinase [Arabidopsis thaliana] >gi 7269298 emb CAB79358.1 (AL161561) putative protein kinase [Arabidops

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1095	LIB3602-058-Q6-K1-A7	7488205	BLASTX	150	2.00E-09	35	probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - <i>Arabidopsis thaliana</i> >gi 5051790 emb CAB45083.1 (AL078637) putative protein kinase [<i>Arabidopsis thaliana</i>] >gi 7269298 emb CAB79358.1 (AL161561) putative protein kinase [<i>Arabidopsis</i>
1096	LIB3602-023-Q6-K1-B3	7630007	BLASTX	783	1.00E-83	89	(AL132960) ribosomal protein S3a homolog [<i>Arabidopsis thaliana</i>]
1097	LIB3602-115-Q1-K1-B10	7630007	BLASTX	737	3.00E-78	89	(AL132960) ribosomal protein S3a homolog [<i>Arabidopsis thaliana</i>]
1098	LIB3602-018-Q6-K1-G12	7630007	BLASTX	722	2.00E-76	88	(AL132960) ribosomal protein S3a homolog [<i>Arabidopsis thaliana</i>]
1099	LIB3602-058-Q6-K1-F9	7630007	BLASTX	708	7.00E-75	89	(AL132960) ribosomal protein S3a homolog [<i>Arabidopsis thaliana</i>]
1100	LIB3602-010-Q6-K1-C7	7630007	BLASTX	695	3.00E-73	89	(AL132960) ribosomal protein S3a homolog [<i>Arabidopsis thaliana</i>]
1101	LIB3602-047-Q6-K1-D9	7630007	BLASTX	665	8.00E-70	89	(AL132960) ribosomal protein S3a homolog [<i>Arabidopsis thaliana</i>]
1102	LIB3602-065-Q1-K6-A10	7630007	BLASTX	664	1.00E-69	91	(AL132960) ribosomal protein S3a homolog [<i>Arabidopsis thaliana</i>]
1103	LIB3602-065-Q1-K6-H1	7630007	BLASTX	632	6.00E-66	86	(AL132960) ribosomal protein S3a homolog [<i>Arabidopsis thaliana</i>]
1104	LIB3602-012-Q6-K1-C6	6729494	BLASTX	680	2.00E-71	78	(AL132966) 60S RIBOSOMAL PROTEIN L12-like [<i>Arabidopsis thaliana</i>]
1105	LIB3602-057-Q6-K1-B6	6729494	BLASTX	680	2.00E-71	78	(AL132966) 60S RIBOSOMAL PROTEIN L12-like [<i>Arabidopsis thaliana</i>]
1106	LIB3602-072-Q1-K1-H8	6729494	BLASTX	667	6.00E-70	78	(AL132966) 60S RIBOSOMAL PROTEIN L12-like [<i>Arabidopsis thaliana</i>]
1107	LIB3602-015-Q6-K1-B5	6729494	BLASTX	448	2.00E-44	75	(AL132966) 60S RIBOSOMAL PROTEIN L12-like [<i>Arabidopsis thaliana</i>]
1108	LIB3602-020-Q6-K1-A4	6729494	BLASTX	399	9.00E-39	74	(AL132966) 60S RIBOSOMAL PROTEIN L12-like [<i>Arabidopsis thaliana</i>]
1109	LIB3602-059-Q6-K1-A1	6729494	BLASTX	285	1.00E-25	65	(AL132966) 60S RIBOSOMAL PROTEIN L12-like [<i>Arabidopsis thaliana</i>]
1110	LIB3602-043-Q6-K1-C5	6729494	BLASTX	176	4.00E-13	64	(AL132966) 60S RIBOSOMAL PROTEIN L12-like [<i>Arabidopsis thaliana</i>]
1111	LIB3602-078-Q6-K6-F12	5762260	BLASTX	693	5.00E-73	75	(AB008848) Csf-3 [<i>Cucumis sativus</i>]
1112	LIB3602-112-Q1-K1-C2	5762260	BLASTX	655	1.00E-68	74	(AB008848) Csf-3 [<i>Cucumis sativus</i>]
1113	LIB3602-093-Q6-K6-E1	5762260	BLASTX	266	5.00E-45	65	(AB008848) Csf-3 [<i>Cucumis sativus</i>]
1114	LIB3602-086-Q6-K1-H5	5762260	BLASTX	312	9.00E-43	74	(AB008848) Csf-3 [<i>Cucumis sativus</i>]
1115	LIB3602-026-Q6-K1-C10	5762260	BLASTX	406	2.00E-39	72	(AB008848) Csf-3 [<i>Cucumis sativus</i>]
1116	LIB3602-088-Q6-K6-B11	5762260	BLASTX	312	1.00E-31	74	(AB008848) Csf-3 [<i>Cucumis sativus</i>]
1117	LIB3602-118-Q1-K1-B11	5762260	BLASTX	206	7.00E-30	70	(AB008848) Csf-3 [<i>Cucumis sativus</i>]
1118	LIB3602-116-Q1-K1-G11	1702984	BLASTX	762	1.00E-100	90	14-3-3-LIKE PROTEIN >gi 1361946 pir S57283 14-3-3 brain protein homolog - <i>Chlamydomonas reinhardtii</i> >gi 1015462 emb CAA55964.1 (X79445) 14-3-3 protein [<i>Chlamydomonas reinhardtii</i>]
1119	LIB3602-094-Q6-K6-G11	1702984	BLASTX	879	2.00E-94	92	14-3-3-LIKE PROTEIN >gi 1361946 pir S57283 14-3-3 brain protein homolog - <i>Chlamydomonas reinhardtii</i> >gi 1015462 emb CAA55964.1 (X79445) 14-3-3 protein [<i>Chlamydomonas reinhardtii</i>]
1120	LIB3602-014-Q6-K1-C8	1702984	BLASTX	725	8.00E-77	96	14-3-3-LIKE PROTEIN >gi 1361946 pir S57283 14-3-3 brain protein homolog - <i>Chlamydomonas reinhardtii</i> >gi 1015462 emb CAA55964.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1121	LIB3602-050-Q6-K1-C10	1702984	BLASTX	331	1.00E-30	96	(X79445) 14-3-3 protein [Chlamydomonas reinhardtii] 14-3-3-LIKE PROTEIN >gi 1361946 pir S57283 14-3-3 brain protein homolog - Chlamydomonas reinhardtii >gi 1015462 emb CAA55964.1 (X79445) 14-3-3 protein [Chlamydomonas reinhardtii]
1122	LIB3602-016-Q6-K1-A9	1702984	BLASTX	291	5.00E-26	98	14-3-3-LIKE PROTEIN >gi 1361946 pir S57283 14-3-3 brain protein homolog - Chlamydomonas reinhardtii >gi 1015462 emb CAA55964.1 (X79445) 14-3-3 protein [Chlamydomonas reinhardtii]
1123	LIB3602-026-Q6-K1-F8	1702984	BLASTX	291	6.00E-26	98	14-3-3-LIKE PROTEIN >gi 1361946 pir S57283 14-3-3 brain protein homolog - Chlamydomonas reinhardtii >gi 1015462 emb CAA55964.1 (X79445) 14-3-3 protein [Chlamydomonas reinhardtii]
1124	LIB3602-048-Q6-K1QA-G12	1702984	BLASTX	277	3.00E-24	98	14-3-3-LIKE PROTEIN >gi 1361946 pir S57283 14-3-3 brain protein homolog - Chlamydomonas reinhardtii >gi 1015462 emb CAA55964.1 (X79445) 14-3-3 protein [Chlamydomonas reinhardtii]
1125	LIB3602-015-Q6-K1-H7	1710565	BLASTX	428	5.00E-42	81	60S RIBOSOMAL PROTEIN L44 (L41) >gi 1255906 dbj BAA11057.1 (D67040) ribosomal protein L41 [Candida utilis]
1126	LIB3602-047-Q6-K1-G7	1710565	BLASTX	377	4.00E-36	83	60S RIBOSOMAL PROTEIN L44 (L41) >gi 1255906 dbj BAA11057.1 (D67040) ribosomal protein L41 [Candida utilis]
1127	LIB3602-090-Q6-K6-A9	1710565	BLASTX	376	7.00E-36	79	60S RIBOSOMAL PROTEIN L44 (L41) >gi 1255906 dbj BAA11057.1 (D67040) ribosomal protein L41 [Candida utilis]
1128	LIB3602-049-Q6-K1-H6	1710565	BLASTX	342	5.00E-32	82	60S RIBOSOMAL PROTEIN L44 (L41) >gi 1255906 dbj BAA11057.1 (D67040) ribosomal protein L41 [Candida utilis]
1129	LIB3602-082-Q6-K6-A2	1710565	BLASTX	234	1.00E-28	74	60S RIBOSOMAL PROTEIN L44 (L41) >gi 1255906 dbj BAA11057.1 (D67040) ribosomal protein L41 [Candida utilis]
1130	LIB3602-048-Q6-K1QA-E5	1710565	BLASTX	282	6.00E-25	62	60S RIBOSOMAL PROTEIN L44 (L41) >gi 1255906 dbj BAA11057.1 (D67040) ribosomal protein L41 [Candida utilis]
1131	LIB3602-088-Q6-K6-F8	1710565	BLASTX	275	5.00E-24	80	60S RIBOSOMAL PROTEIN L44 (L41) >gi 1255906 dbj BAA11057.1 (D67040) ribosomal protein L41 [Candida utilis]
1132	LIB3602-107-Q1-K1-C8	119167	BLASTX	415	1.00E-40	83	ELONGATION FACTOR 2 (EF-2) >gi 421771 pir S32819 translation elongation factor eEF-2 - Chlorella kessleri >gi 167245 gb AAA33028.1 (M68064) elongation factor 2 [Chlorella kessleri] >gi 228693 prf 1808323A elongation factor 2 [Chlorella kessleri]
1133	LIB3602-021-Q6-K1-D11	119167	BLASTX	400	3.00E-39	91	ELONGATION FACTOR 2 (EF-2) >gi 421771 pir S32819 translation elongation factor eEF-2 - Chlorella kessleri >gi 167245 gb AAA33028.1 (M68064) elongation factor 2 [Chlorella kessleri] >gi 228693 prf 1808323A elongation factor 2 [Chlorella kessleri]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1134	LIB3602-086-Q6-K1-C8	119167	BLASTX	372	2.00E-35	58	ELONGATION FACTOR 2 (EF-2) >gi 421771 pir S32819 translation elongation factor eEF-2 - Chlorella kessleri >gi 167245 gb AAA33028.1 (M68064) elongation factor 2 [Chlorella kessleri] >gi 228693 prf 1808323A elongation factor 2 [Chlorella kessleri]
1135	LIB3602-071-Q1-K1-A12	119167	BLASTX	338	1.00E-31	79	ELONGATION FACTOR 2 (EF-2) >gi 421771 pir S32819 translation elongation factor eEF-2 - Chlorella kessleri >gi 167245 gb AAA33028.1 (M68064) elongation factor 2 [Chlorella kessleri] >gi 228693 prf 1808323A elongation factor 2 [Chlorella kessleri]
1136	LIB3602-066-Q1-K6-A12	119167	BLASTX	318	3.00E-29	76	ELONGATION FACTOR 2 (EF-2) >gi 421771 pir S32819 translation elongation factor eEF-2 - Chlorella kessleri >gi 167245 gb AAA33028.1 (M68064) elongation factor 2 [Chlorella kessleri] >gi 228693 prf 1808323A elongation factor 2 [Chlorella kessleri]
1137	LIB3602-014-Q6-K1-C3	119167	BLASTX	215	2.00E-17	78	ELONGATION FACTOR 2 (EF-2) >gi 421771 pir S32819 translation elongation factor eEF-2 - Chlorella kessleri >gi 167245 gb AAA33028.1 (M68064) elongation factor 2 [Chlorella kessleri] >gi 228693 prf 1808323A elongation factor 2 [Chlorella kessleri]
1138	LIB3602-014-Q6-K1-E6	119167	BLASTX	170	1.00E-11	41	ELONGATION FACTOR 2 (EF-2) >gi 421771 pir S32819 translation elongation factor eEF-2 - Chlorella kessleri >gi 167245 gb AAA33028.1 (M68064) elongation factor 2 [Chlorella kessleri] >gi 228693 prf 1808323A elongation factor 2 [Chlorella kessleri]
1139	LIB3602-076-Q6-K6-E12	6225750	BLASTX	524	3.00E-53	68	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (NDPK I) >gi 3309053 gb AAC25999.1 (AF072289) nucleoside diphosphate kinase I [Mesembryanthemum crystallinum]
1140	LIB3602-092-Q6-K6-D6	6225750	BLASTX	524	3.00E-53	68	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (NDPK I) >gi 3309053 gb AAC25999.1 (AF072289) nucleoside diphosphate kinase I [Mesembryanthemum crystallinum]
1141	LIB3602-115-Q1-K1-H3	6225750	BLASTX	427	8.00E-42	68	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (NDPK I) >gi 3309053 gb AAC25999.1 (AF072289) nucleoside diphosphate kinase I [Mesembryanthemum crystallinum]
1142	LIB3602-114-Q1-K1-B8	6225750	BLASTX	378	5.00E-36	73	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (NDPK I) >gi 3309053 gb AAC25999.1 (AF072289) nucleoside diphosphate kinase I [Mesembryanthemum crystallinum]
1143	LIB3602-105-Q1-K1-F6	6225750	BLASTX	281	1.00E-24	69	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (NDPK I) >gi 3309053 gb AAC25999.1 (AF072289)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1144	LIB3602-062-Q6-K1-F1	6225750	BLASTX	262	1.00E-22	68	nucleoside diphosphate kinase I [Mesembryanthemum crystallinum] NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (NDPK I) >gi 3309053 gb AAC25999.1 (AF072289)
1145	LIB3602-093-Q6-K6-B8	6225750	BLASTX	152	1.00E-09	53	nucleoside diphosphate kinase I [Mesembryanthemum crystallinum] NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (NDPK I) >gi 3309053 gb AAC25999.1 (AF072289)
1146	LIB3602-062-Q6-K1-E12	7461899	BLASTX	580	8.00E-60	62	nucleoside diphosphate kinase I [Mesembryanthemum crystallinum] translation elongation factor EF-3 homolog A666L - Chlorella virus PBCV-1 >gi 2447123 gb AAC96981.1 (U42580) Chlorella virus CVK2 translation elongation factor-3 homolog, refer to GenBank Accession Number D16505 [Paramecium bursaria Chlorella virus 1]
1147	LIB3602-066-Q1-K6-G12	7461899	BLASTX	511	1.00E-51	59	translation elongation factor EF-3 homolog A666L - Chlorella virus PBCV-1 >gi 2447123 gb AAC96981.1 (U42580) Chlorella virus CVK2 translation elongation factor-3 homolog, refer to GenBank Accession Number D16505 [Paramecium bursaria Chlorella virus 1]
1148	LIB3602-009-Q6-K1-C12	7461899	BLASTX	459	1.00E-45	51	translation elongation factor EF-3 homolog A666L - Chlorella virus PBCV-1 >gi 2447123 gb AAC96981.1 (U42580) Chlorella virus CVK2 translation elongation factor-3 homolog, refer to GenBank Accession Number D16505 [Paramecium bursaria Chlorella virus 1]
1149	LIB3602-045-Q6-K1-A7	7461899	BLASTX	435	7.00E-43	61	translation elongation factor EF-3 homolog A666L - Chlorella virus PBCV-1 >gi 2447123 gb AAC96981.1 (U42580) Chlorella virus CVK2 translation elongation factor-3 homolog, refer to GenBank Accession Number D16505 [Paramecium bursaria Chlorella virus 1]
1150	LIB3602-089-Q6-K6-A1	7461899	BLASTX	336	4.00E-38	45	translation elongation factor EF-3 homolog A666L - Chlorella virus PBCV-1 >gi 2447123 gb AAC96981.1 (U42580) Chlorella virus CVK2 translation elongation factor-3 homolog, refer to GenBank Accession Number D16505 [Paramecium bursaria Chlorella virus 1]
1151	LIB3602-029-Q6-K1-G9	7461899	BLASTX	269	2.00E-23	43	translation elongation factor EF-3 homolog A666L - Chlorella virus PBCV-1 >gi 2447123 gb AAC96981.1 (U42580) Chlorella virus CVK2 translation elongation factor-3 homolog, refer to GenBank Accession Number D16505 [Paramecium bursaria Chlorella virus 1]
1152	LIB3602-059-Q6-K1-G9	7461899	BLASTX	153	7.00E-10	33	translation elongation factor EF-3 homolog A666L - Chlorella virus PBCV-1 >gi 2447123 gb AAC96981.1 (U42580) Chlorella virus CVK2 translation elongation factor-3 homolog, refer to GenBank Accession Number D16505 [Paramecium bursaria Chlorella virus 1]
1153	LIB3602-029-Q6-K1-F12	7268983	BLASTX	638	1.00E-66	74	(AL161494) putative ribosomal protein L19 [Arabidopsis thaliana]
1154	LIB3602-008-Q6-K1-A5	7268983	BLASTX	631	8.00E-66	74	(AL161494) putative ribosomal protein L19 [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1155	LIB3602-070-Q1-K1-C3	7268983	BLASTX	582	5.00E-60	72	(AL161494) putative ribosomal protein L19 [Arabidopsis thaliana]
1156	LIB3602-088-Q6-K6-E1	7268983	BLASTX	516	3.00E-52	64	(AL161494) putative ribosomal protein L19 [Arabidopsis thaliana]
1157	LIB3602-008-Q6-K1-F11	7268983	BLASTX	432	2.00E-42	70	(AL161494) putative ribosomal protein L19 [Arabidopsis thaliana]
1158	LIB3602-083-Q6-K6-E9	7268983	BLASTX	297	1.00E-26	66	(AL161494) putative ribosomal protein L19 [Arabidopsis thaliana]
1159	LIB3602-051-Q6-K1-C3	7268983	BLASTX	175	7.00E-14	73	(AL161494) putative ribosomal protein L19 [Arabidopsis thaliana]
1160	LIB3602-019-Q6-K1-G12	6525246	BLASTX	200	1.00E-15	57	(U12390) beta-galactosidase alpha peptide [Cloning vector pSport1]
1161	LIB3602-040-Q6-K1-F7	6525246	BLASTX	171	4.00E-12	52	(U12390) beta-galactosidase alpha peptide [Cloning vector pSport1]
1162	LIB3602-037-Q6-K1-B7	6525246	BLASTX	166	1.00E-11	54	(U12390) beta-galactosidase alpha peptide [Cloning vector pSport1]
1163	LIB3602-013-Q6-K1-A12	6525246	BLASTX	163	3.00E-11	45	(U12390) beta-galactosidase alpha peptide [Cloning vector pSport1]
1164	LIB3602-118-Q1-K1-B6	6525246	BLASTX	161	6.00E-11	46	(U12390) beta-galactosidase alpha peptide [Cloning vector pSport1]
1165	LIB3602-047-Q6-K1-B6	6525246	BLASTX	158	2.00E-10	45	(U12390) beta-galactosidase alpha peptide [Cloning vector pSport1]
1166	LIB3602-011-Q6-K1-F12	541546	BLASTX	850	1.00E-91	98	polyubiquitin 5 - Volvox carteri >gi 395295 emb CAA52290.1 (X74214) polyubiquitin [Volvox carteri]
1167	LIB3602-045-Q6-K1-E12	541546	BLASTX	763	2.00E-81	99	polyubiquitin 5 - Volvox carteri >gi 395295 emb CAA52290.1 (X74214) polyubiquitin [Volvox carteri]
1168	LIB3602-030-Q6-K1-F7	541546	BLASTX	762	3.00E-81	100	polyubiquitin 5 - Volvox carteri >gi 395295 emb CAA52290.1 (X74214) polyubiquitin [Volvox carteri]
1169	LIB3602-061-Q6-K1-D11	541546	BLASTX	670	2.00E-70	98	polyubiquitin 5 - Volvox carteri >gi 395295 emb CAA52290.1 (X74214) polyubiquitin [Volvox carteri]
1170	LIB3602-030-Q6-K1-D10	541546	BLASTX	662	2.00E-69	100	polyubiquitin 5 - Volvox carteri >gi 395295 emb CAA52290.1 (X74214) polyubiquitin [Volvox carteri]
1171	LIB3602-063-Q1-K6-B2	541546	BLASTX	515	3.00E-52	99	polyubiquitin 5 - Volvox carteri >gi 395295 emb CAA52290.1 (X74214) polyubiquitin [Volvox carteri]
1172	LIB3602-027-Q6-K1-G7	7413634	BLASTX	342	4.00E-32	72	(AL162971) 60S ribosomal protein-like [Arabidopsis thaliana]
1173	LIB3602-022-Q6-K1-B11	7413634	BLASTX	342	5.00E-32	72	(AL162971) 60S ribosomal protein-like [Arabidopsis thaliana]
1174	LIB3602-060-Q6-K1-G4	7413634	BLASTX	342	6.00E-32	72	(AL162971) 60S ribosomal protein-like [Arabidopsis thaliana]
1175	LIB3602-043-Q6-K1-C11	7413634	BLASTX	342	6.00E-32	72	(AL162971) 60S ribosomal protein-like [Arabidopsis thaliana]
1176	LIB3602-034-Q6-K1-D7	7413634	BLASTX	272	6.00E-24	76	(AL162971) 60S ribosomal protein-like [Arabidopsis thaliana]
1177	LIB3602-094-Q6-K6-E8	7413634	BLASTX	219	1.00E-17	86	(AL162971) 60S ribosomal protein-like [Arabidopsis thaliana]
1178	LIB3602-030-Q6-K1-H12	7486582	BLASTX	229	9.00E-19	43	hypothetical protein F7H19.70 - Arabidopsis thaliana >gi 3292814 emb CAA19804.1 (AL031018) putative protein [Arabidopsis thaliana] >gi 7269136 emb CAB79244.1 (AL161558) putative protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1179	LIB3602-105-Q1-K1-H3	7486582	BLASTX	224	5.00E-18	50	hypothetical protein F7H19.70 - Arabidopsis thaliana >gi 3292814 emb CAA19804.1 (AL031018) putative protein [Arabidopsis thaliana] >gi 7269136 emb CAB79244.1 (AL161558) putative protein [Arabidopsis thaliana]
1180	LIB3602-058-Q6-K1-E5	7486582	BLASTX	223	5.00E-18	41	hypothetical protein F7H19.70 - Arabidopsis thaliana >gi 3292814 emb CAA19804.1 (AL031018) putative protein [Arabidopsis thaliana] >gi 7269136 emb CAB79244.1 (AL161558) putative protein [Arabidopsis thaliana]
1181	LIB3602-114-Q1-K1-H7	7486582	BLASTX	217	3.00E-17	35	hypothetical protein F7H19.70 - Arabidopsis thaliana >gi 3292814 emb CAA19804.1 (AL031018) putative protein [Arabidopsis thaliana] >gi 7269136 emb CAB79244.1 (AL161558) putative protein [Arabidopsis thaliana]
1182	LIB3602-084-Q6-K1-G8	7486582	BLASTX	190	4.00E-14	58	hypothetical protein F7H19.70 - Arabidopsis thaliana >gi 3292814 emb CAA19804.1 (AL031018) putative protein [Arabidopsis thaliana] >gi 7269136 emb CAB79244.1 (AL161558) putative protein [Arabidopsis thaliana]
1183	LIB3602-062-Q6-K1-A2	7486582	BLASTX	164	4.00E-11	56	hypothetical protein F7H19.70 - Arabidopsis thaliana >gi 3292814 emb CAA19804.1 (AL031018) putative protein [Arabidopsis thaliana] >gi 7269136 emb CAB79244.1 (AL161558) putative protein [Arabidopsis thaliana]
1184	LIB3602-068-Q1-K1-F1	7486992	BLASTX	316	9.00E-29	42	hypothetical protein T13L16.5 - Arabidopsis thaliana >gi 6598526 gb AAD20114.2 (AC006201) hypothetical protein [Arabidopsis thaliana]
1185	LIB3602-009-Q6-K1-F7	7486992	BLASTX	244	2.00E-20	38	hypothetical protein T13L16.5 - Arabidopsis thaliana >gi 6598526 gb AAD20114.2 (AC006201) hypothetical protein [Arabidopsis thaliana]
1186	LIB3602-057-Q6-K1-F3	7486992	BLASTX	185	3.00E-18	35	hypothetical protein T13L16.5 - Arabidopsis thaliana >gi 6598526 gb AAD20114.2 (AC006201) hypothetical protein [Arabidopsis thaliana]
1187	LIB3602-085-Q6-K1-C5	7486992	BLASTX	218	2.00E-17	35	hypothetical protein T13L16.5 - Arabidopsis thaliana >gi 6598526 gb AAD20114.2 (AC006201) hypothetical protein [Arabidopsis thaliana]
1188	LIB3602-086-Q6-K1-C6	7486992	BLASTX	193	2.00E-14	34	hypothetical protein T13L16.5 - Arabidopsis thaliana >gi 6598526 gb AAD20114.2 (AC006201) hypothetical protein [Arabidopsis thaliana]
1189	LIB3602-089-Q6-K6-H12	7486992	BLASTX	177	1.00E-12	36	hypothetical protein T13L16.5 - Arabidopsis thaliana >gi 6598526 gb AAD20114.2 (AC006201) hypothetical protein [Arabidopsis thaliana]
1190	LIB3602-070-Q1-K1-B2	7441117	BLASTX	766	1.00E-81	77	ribosomal protein S3a, cytosolic - Arabidopsis thaliana >gi 2661422 emb CAA04689.1 (AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1 (AL023094) Putative S-phase-specific ribosomal protein [Arabidops
1191	LIB3602-043-Q6-K1-A9	7441117	BLASTX	654	2.00E-68	78	ribosomal protein S3a, cytosolic - Arabidopsis thaliana >gi 2661422 emb CAA04689.1 (AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1 (AL023094) Putative S-phase-specific ribosomal protein [Arabidops

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1192	LIB3602-081-Q6-K6-H1	7441117	BLASTX	633	6.00E-66	71	ribosomal protein S3a, cytosolic - Arabidopsis thaliana >gi 2661422 emb CAA04689.1 (AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1 (AL023094) Putative S-phase-specific ribosomal protein [Arabidops
1193	LIB3602-070-Q1-K1-G11	7441117	BLASTX	600	4.00E-62	71	ribosomal protein S3a, cytosolic - Arabidopsis thaliana >gi 2661422 emb CAA04689.1 (AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1 (AL023094) Putative S-phase-specific ribosomal protein [Arabidops
1194	LIB3602-044-Q6-K1-H3	7441117	BLASTX	520	8.00E-53	81	ribosomal protein S3a, cytosolic - Arabidopsis thaliana >gi 2661422 emb CAA04689.1 (AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1 (AL023094) Putative S-phase-specific ribosomal protein [Arabidops
1195	LIB3602-054-Q6-K1-F8	7441117	BLASTX	473	2.00E-47	81	ribosomal protein S3a, cytosolic - Arabidopsis thaliana >gi 2661422 emb CAA04689.1 (AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1 (AL023094) Putative S-phase-specific ribosomal protein [Arabidops
1196	LIB3602-046-Q6-K1-C2	1710530	BLASTX	577	2.00E-59	71	60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256 ribosomal protein L27a, cytosolic - Arabidopsis thaliana >gi 1107487 emb CAA63025.1 (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana] >gi 6175150 gb AAF04877.1 AC010796_13 (AC010796) 60S ribosom
1197	LIB3602-049-Q6-K1-E3	1710530	BLASTX	563	8.00E-58	71	60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256 ribosomal protein L27a, cytosolic - Arabidopsis thaliana >gi 1107487 emb CAA63025.1 (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana] >gi 6175150 gb AAF04877.1 AC010796_13 (AC010796) 60S ribosom
1198	LIB3602-062-Q6-K1-B1	1710530	BLASTX	339	1.00E-31	62	60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256 ribosomal protein L27a, cytosolic - Arabidopsis thaliana >gi 1107487 emb CAA63025.1 (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana] >gi 6175150 gb AAF04877.1 AC010796_13 (AC010796) 60S ribosom
1199	LIB3602-120-Q1-K1-F11	1710530	BLASTX	160	3.00E-22	68	60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256 ribosomal protein L27a, cytosolic - Arabidopsis thaliana >gi 1107487 emb CAA63025.1 (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana] >gi 6175150 gb AAF04877.1 AC010796_13 (AC010796) 60S ribosom
1200	LIB3602-113-Q1-K1-F11	1710530	BLASTX	258	4.00E-22	56	60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256 ribosomal protein L27a,

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1201	LIB3602-119-Q1-K1-B11	1710530	BLASTX	189	1.00E-14	71	cytosolic - Arabidopsis thaliana >gi 1107487 emb CAA63025.1 (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana] >gi 6175150 gb AAF04877.1 AC010796_13 (AC010796) 60S ribosom 60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256 ribosomal protein L27a, cytosolic - Arabidopsis thaliana >gi 1107487 emb CAA63025.1 (X91959) 60S ribosomal protein L27a [Arabidopsis thaliana] >gi 6175150 gb AAF04877.1 AC010796_13 (AC010796) 60S ribosom
1202	LIB3602-077-Q6-K6-E7	4139222	BLASTX	353	4.00E-33	59	(AF104633) light harvesting complex I protein precursor [Chlamydomonas reinhardtii]
1203	LIB3602-076-Q6-K6-G3	4139222	BLASTX	344	4.00E-32	56	(AF104633) light harvesting complex I protein precursor [Chlamydomonas reinhardtii]
1204	LIB3602-048-Q6-K1QA-H3	4139222	BLASTX	299	6.00E-27	57	(AF104633) light harvesting complex I protein precursor [Chlamydomonas reinhardtii]
1205	LIB3602-113-Q1-K1-A4	4139222	BLASTX	208	1.00E-17	72	(AF104633) light harvesting complex I protein precursor [Chlamydomonas reinhardtii]
1206	LIB3602-013-Q6-K1-H4	4139222	BLASTX	213	7.00E-17	63	(AF104633) light harvesting complex I protein precursor [Chlamydomonas reinhardtii]
1207	LIB3602-105-Q1-K1-E12	4139222	BLASTX	181	2.00E-16	70	(AF104633) light harvesting complex I protein precursor [Chlamydomonas reinhardtii]
1208	LIB3602-011-Q6-K1-B4	5758041	BLASTX	303	3.00E-27	49	(AF133814) ferritin 1 [Solanum tuberosum]
1209	LIB3602-018-Q6-K1-A6	5758041	BLASTX	303	3.00E-27	49	(AF133814) ferritin 1 [Solanum tuberosum]
1210	LIB3602-001-P1-K6-B3	5758041	BLASTX	303	3.00E-27	49	(AF133814) ferritin 1 [Solanum tuberosum]
1211	LIB3602-014-Q6-K1-A11	5758041	BLASTX	295	2.00E-26	50	(AF133814) ferritin 1 [Solanum tuberosum]
1212	LIB3602-107-Q1-K1-E12	5758041	BLASTX	275	5.00E-24	49	(AF133814) ferritin 1 [Solanum tuberosum]
1213	LIB3602-051-Q6-K1-D11	5758041	BLASTX	148	3.00E-21	45	(AF133814) ferritin 1 [Solanum tuberosum]
1214	LIB3602-020-Q6-K1-H3	3122724	BLASTX	289	6.00E-26	81	60S RIBOSOMAL PROTEIN L38 >gi 2289009 gb AAB64338.1 (AC002335) 60S ribosomal protein L38 [Arabidopsis thaliana] >gi 6996290 emb CAB75451.1 (AL138659) 60S RIBOSOMAL PROTEIN L38-like protein [Arabidopsis thaliana]
1215	LIB3602-072-Q1-K1-E10	3122724	BLASTX	283	3.00E-25	79	60S RIBOSOMAL PROTEIN L38 >gi 2289009 gb AAB64338.1 (AC002335) 60S ribosomal protein L38 [Arabidopsis thaliana] >gi 6996290 emb CAB75451.1 (AL138659) 60S RIBOSOMAL PROTEIN L38-like protein [Arabidopsis thaliana]
1216	LIB3602-100-Q1-K1-A5	3122724	BLASTX	158	1.00E-20	79	60S RIBOSOMAL PROTEIN L38 >gi 2289009 gb AAB64338.1 (AC002335) 60S ribosomal protein L38 [Arabidopsis thaliana] >gi 6996290 emb CAB75451.1 (AL138659) 60S RIBOSOMAL PROTEIN L38-like protein [Arabidopsis thaliana]
1217	LIB3602-067-Q1-K1-A12	3122724	BLASTX	244	2.00E-20	79	60S RIBOSOMAL PROTEIN L38 >gi 2289009 gb AAB64338.1 (AC002335) 60S ribosomal protein L38 [Arabidopsis thaliana] >gi 6996290 emb CAB75451.1 (AL138659) 60S RIBOSOMAL PROTEIN L38-like protein [Arabidopsis thaliana]
1218	LIB3602-108-Q1-K1-A5	3122724	BLASTX	148	2.00E-19	81	60S RIBOSOMAL PROTEIN L38 >gi 2289009 gb AAB64338.1 (AC002335) 60S ribosomal protein L38 [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1219	LIB3602-020-Q6-K1-G5	3122724	BLASTX	155	1.00E-10	82	>gi 6996290 emb CAB75451.1 (AL138659) 60S RIBOSOMAL PROTEIN L38-like protein [Arabidopsis thaliana] >gi 2289009 gb AAB64338.1 (AC002335) 60S ribosomal protein L38 [Arabidopsis thaliana] >gi 6996290 emb CAB75451.1 (AL138659) 60S RIBOSOMAL PROTEIN L38-like protein [Arabidopsis thaliana]
1220	LIB3602-066-Q1-K6-H8	132100	BLASTX	570	1.00E-58	66	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3 PRECURSOR (RUBISCO SMALL SUBUNIT 3) >gi 68108 pir RKJK3C ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain 3 precursor - Acetabularia cliftonii >gi 732546 emb CAA36105.1 (X51808) ribulose bisphos
1221	LIB3602-049-Q6-K1-G9	132100	BLASTX	556	5.00E-57	66	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3 PRECURSOR (RUBISCO SMALL SUBUNIT 3) >gi 68108 pir RKJK3C ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain 3 precursor - Acetabularia cliftonii >gi 732546 emb CAA36105.1 (X51808) ribulose bisphos
1222	LIB3602-012-Q6-K1-G3	132100	BLASTX	546	9.00E-56	68	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3 PRECURSOR (RUBISCO SMALL SUBUNIT 3) >gi 68108 pir RKJK3C ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain 3 precursor - Acetabularia cliftonii >gi 732546 emb CAA36105.1 (X51808) ribulose bisphos
1223	LIB3602-005-Q1-K1-E10	132100	BLASTX	520	1.00E-52	68	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3 PRECURSOR (RUBISCO SMALL SUBUNIT 3) >gi 68108 pir RKJK3C ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain 3 precursor - Acetabularia cliftonii >gi 732546 emb CAA36105.1 (X51808) ribulose bisphos
1224	LIB3602-100-Q1-K1-A12	132100	BLASTX	502	1.00E-50	69	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3 PRECURSOR (RUBISCO SMALL SUBUNIT 3) >gi 68108 pir RKJK3C ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain 3 precursor - Acetabularia cliftonii >gi 732546 emb CAA36105.1 (X51808) ribulose bisphos
1225	LIB3602-018-Q6-K1-F5	132100	BLASTX	454	5.00E-45	68	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3 PRECURSOR (RUBISCO SMALL SUBUNIT 3) >gi 68108 pir RKJK3C ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain 3 precursor - Acetabularia cliftonii >gi 732546 emb CAA36105.1 (X51808) ribulose bisphos
1226	LIB3602-017-Q6-K1-A9	1709786	BLASTX	377	5.00E-36	55	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi 541894 pir JQ2334 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Arabidopsis thaliana >gi 166815 gb AAA61346.1 (M76538) pyrroline carboxylate reductase [Arabidopsis thaliana] >gi 1632776 emb

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1227	LIB3602-006-Q1-K1-A2	1709786	BLASTX	369	5.00E-35	68	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi 541894 pir JQ2334 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Arabidopsis thaliana >gi 166815 gb AAA61346.1 (M76538) pyrroline carboxylate reductase [Arabidopsis thaliana] >gi 1632776 emb
1228	LIB3602-106-Q1-K1-C9	1709786	BLASTX	288	2.00E-25	55	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi 541894 pir JQ2334 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Arabidopsis thaliana >gi 166815 gb AAA61346.1 (M76538) pyrroline carboxylate reductase [Arabidopsis thaliana] >gi 1632776 emb
1229	LIB3602-060-Q6-K1-C1	1709786	BLASTX	230	4.00E-19	61	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi 541894 pir JQ2334 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Arabidopsis thaliana >gi 166815 gb AAA61346.1 (M76538) pyrroline carboxylate reductase [Arabidopsis thaliana] >gi 1632776 emb
1230	LIB3602-046-Q6-K1-F7	1709786	BLASTX	206	5.00E-16	67	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi 541894 pir JQ2334 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Arabidopsis thaliana >gi 166815 gb AAA61346.1 (M76538) pyrroline carboxylate reductase [Arabidopsis thaliana] >gi 1632776 emb
1231	LIB3602-007-Q1-K1-G11	1709786	BLASTX	158	3.00E-10	34	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi 541894 pir JQ2334 pyrroline-5-carboxylate reductase (EC 1.5.1.2) - Arabidopsis thaliana >gi 166815 gb AAA61346.1 (M76538) pyrroline carboxylate reductase [Arabidopsis thaliana] >gi 1632776 emb
1232	LIB3602-017-Q6-K1-B10	4590398	BLASTX	387	3.00E-37	71	(AF124243) ribosomal protein homolog [Cryptosporidium parvum]
1233	LIB3602-109-Q1-K1-G11	4590398	BLASTX	207	7.00E-31	68	(AF124243) ribosomal protein homolog [Cryptosporidium parvum]
1234	LIB3602-109-Q1-K1-D2	4590398	BLASTX	218	5.00E-29	70	(AF124243) ribosomal protein homolog [Cryptosporidium parvum]
1235	LIB3602-006-Q1-K1-F4	4590398	BLASTX	309	3.00E-28	65	(AF124243) ribosomal protein homolog [Cryptosporidium parvum]
1236	LIB3602-009-Q6-K1-A8	4590398	BLASTX	302	2.00E-27	69	(AF124243) ribosomal protein homolog [Cryptosporidium parvum]
1237	LIB3602-049-Q6-K1-C4	1168732	BLASTX	378	4.00E-36	60	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 421914 pir S28045 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) ELI3 - parsley (fragment) >gi 836638 emb CAA48028.1 (X67817) Eli3 [Petroselinum crispum]
1238	LIB3602-038-Q6-K1-C5	1168732	BLASTX	249	1.00E-34	57	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 421914 pir S28045 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) ELI3 - parsley (fragment) >gi 836638 emb CAA48028.1 (X67817) Eli3 [Petroselinum crispum]
1239	LIB3602-038-Q6-K1-C4	1168732	BLASTX	249	1.00E-34	57	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 421914 pir S28045 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) ELI3 - parsley

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1240	LIB3602-067-Q1-K1-A6	1168732	BLASTX	304	2.00E-27	56	(fragment) >gi 836638 emb CAA48028.1 (X67817) Eli3 [Petroselinum crispum] CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 421914 pir S28045 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) ELI3 - parsley (fragment) >gi 836638 emb CAA48028.1 (X67817) Eli3 [Petroselinum crispum]
1241	LIB3602-001-P1-K6-B6	1168732	BLASTX	301	4.00E-27	57	CINNAMYL-ALCOHOL DEHYDROGENASE (CAD) >gi 421914 pir S28045 cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) ELI3 - parsley (fragment) >gi 836638 emb CAA48028.1 (X67817) Eli3 [Petroselinum crispum]
1242	LIB3602-006-Q1-K1-D4	7443234	BLASTX	364	2.00E-34	50	light harvesting complex A protein precursor - Volvox carteri >gi 732534 gb AAB40979.1 (U22329) light harvesting complex a [Volvox carteri]
1243	LIB3602-090-Q6-K6-E6	7443234	BLASTX	335	5.00E-31	52	light harvesting complex A protein precursor - Volvox carteri >gi 732534 gb AAB40979.1 (U22329) light harvesting complex a [Volvox carteri]
1244	LIB3602-070-Q1-K1-G4	7443234	BLASTX	237	4.00E-21	52	light harvesting complex A protein precursor - Volvox carteri >gi 732534 gb AAB40979.1 (U22329) light harvesting complex a [Volvox carteri]
1245	LIB3602-091-Q6-K6-E1	7443234	BLASTX	230	3.00E-19	52	light harvesting complex A protein precursor - Volvox carteri >gi 732534 gb AAB40979.1 (U22329) light harvesting complex a [Volvox carteri]
1246	LIB3602-105-Q1-K1-A9	7443234	BLASTX	225	4.00E-18	62	light harvesting complex A protein precursor - Volvox carteri >gi 732534 gb AAB40979.1 (U22329) light harvesting complex a [Volvox carteri]
1247	LIB3602-015-Q6-K1-A1	7430859	BLASTX	228	1.00E-18	47	glutaredoxin - rice >gi 2114207 dbj BAA20071.1 (D86744) glutaredoxin [Oryza sativa]
1248	LIB3602-068-Q1-K1-D5	7430859	BLASTX	228	1.00E-18	47	glutaredoxin - rice >gi 2114207 dbj BAA20071.1 (D86744) glutaredoxin [Oryza sativa]
1249	LIB3602-006-Q1-K1-G7	7430859	BLASTX	228	2.00E-18	47	glutaredoxin - rice >gi 2114207 dbj BAA20071.1 (D86744) glutaredoxin [Oryza sativa]
1250	LIB3602-079-Q6-K6-E5	7430859	BLASTX	228	2.00E-18	47	glutaredoxin - rice >gi 2114207 dbj BAA20071.1 (D86744) glutaredoxin [Oryza sativa]
1251	LIB3602-074-Q1-K1-H6	7430859	BLASTX	152	1.00E-11	41	glutaredoxin - rice >gi 2114207 dbj BAA20071.1 (D86744) glutaredoxin [Oryza sativa]
1252	LIB3602-005-Q1-K1-A8	927428	BLASTX	658	3.00E-71	68	(X86733) fis1 [Linum usitatissimum]
1253	LIB3602-010-Q6-K1-B9	927428	BLASTX	671	2.00E-70	69	(X86733) fis1 [Linum usitatissimum]
1254	LIB3602-025-Q6-K1-F4	927428	BLASTX	487	6.00E-49	73	(X86733) fis1 [Linum usitatissimum]
1255	LIB3602-070-Q1-K1-B7	927428	BLASTX	487	7.00E-49	73	(X86733) fis1 [Linum usitatissimum]
1256	LIB3602-047-Q6-K1-E12	927428	BLASTX	431	2.00E-42	76	(X86733) fis1 [Linum usitatissimum]
1257	LIB3602-093-Q6-K6-A5	6730739	BLASTX	300	6.00E-27	55	(AC018849) hypothetical protein [Arabidopsis thaliana]
1258	LIB3602-113-Q1-K1-F5	6730739	BLASTX	300	6.00E-27	55	(AC018849) hypothetical protein [Arabidopsis thaliana]
1259	LIB3602-015-Q6-K1-H8	6730739	BLASTX	240	4.00E-20	47	(AC018849) hypothetical protein [Arabidopsis thaliana]
1260	LIB3602-017-Q6-K1-C5	6730739	BLASTX	171	4.00E-12	60	(AC018849) hypothetical protein [Arabidopsis thaliana]
1261	LIB3602-043-Q6-K1-C10	6730739	BLASTX	145	4.00E-09	55	(AC018849) hypothetical protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1262	LIB3602-042-Q6-K1-F12	3075487	BLASTN	41	2.00E-13	91	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds
1263	LIB3602-093-Q6-K6-A3	3075487	BLASTN	41	2.00E-13	91	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds
1264	LIB3602-049-Q6-K1-H11	3075487	BLASTN	39	3.00E-12	91	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds
1265	LIB3602-056-Q6-K1-G10	3075487	BLASTN	37	5.00E-11	90	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds
1266	LIB3602-104-Q1-K1-A3	3075487	BLASTN	34	3.00E-09	90	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds
1267	LIB3602-039-Q6-K1-G4	100524	BLASTX	768	8.00E-82	98	polyubiquitin 6 - common sunflower >gi 18824 emb CAA40324.1 (X57004) hexaubiquitin protein [Helianthus annuus] >gi 1204096 emb CAA40325.1 (X57005) hexaubiquitin protein [Helianthus annuus]
1268	LIB3602-112-Q1-K1-A9	100524	BLASTX	700	7.00E-74	96	polyubiquitin 6 - common sunflower >gi 18824 emb CAA40324.1 (X57004) hexaubiquitin protein [Helianthus annuus] >gi 1204096 emb CAA40325.1 (X57005) hexaubiquitin protein [Helianthus annuus]
1269	LIB3602-023-Q6-K1-C1	100524	BLASTX	537	7.00E-55	99	polyubiquitin 6 - common sunflower >gi 18824 emb CAA40324.1 (X57004) hexaubiquitin protein [Helianthus annuus] >gi 1204096 emb CAA40325.1 (X57005) hexaubiquitin protein [Helianthus annuus]
1270	LIB3602-116-Q1-K1-G10	100524	BLASTX	226	8.00E-36	95	polyubiquitin 6 - common sunflower >gi 18824 emb CAA40324.1 (X57004) hexaubiquitin protein [Helianthus annuus] >gi 1204096 emb CAA40325.1 (X57005) hexaubiquitin protein [Helianthus annuus]
1271	LIB3602-089-Q6-K6-G10	100524	BLASTX	265	3.00E-35	98	polyubiquitin 6 - common sunflower >gi 18824 emb CAA40324.1 (X57004) hexaubiquitin protein [Helianthus annuus] >gi 1204096 emb CAA40325.1 (X57005) hexaubiquitin protein [Helianthus annuus]
1272	LIB3602-071-Q1-K1-D5	131382	BLASTX	751	8.00E-80	72	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) >gi 81252 pir S05508 photosystem II oxygen-evolving complex protein 1 precursor - Chlamydomonas reinhardtii >gi 18160 emb CAA32053.1 (X13826) OEE1 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1273	LIB3602-010-Q6-K1-C9	131382	BLASTX	665	8.00E-70	72	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) >gi 81252 pir S05508 photosystem II oxygen-evolving complex protein 1 precursor - Chlamydomonas reinhardtii >gi 18160 emb CAA32053.1 (X13826) OEE1 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1274	LIB3602-058-Q6-K1-G8	131382	BLASTX	647	1.00E-67	73	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) >gi 81252 pir S05508 photosystem II oxygen-evolving complex protein 1 precursor - Chlamydomonas reinhardtii >gi 18160 emb CAA32053.1 (X13826) OEE1 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1275	LIB3602-043-Q6-K1-F10	131382	BLASTX	434	6.00E-43	67	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) >gi 81252 pir S05508

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							photosystem II oxygen-evolving complex protein 1 precursor - Chlamydomonas reinhardtii >gi 18160 emb CAA32053.1 (X13826) OEE1 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1276	LIB3602-070-Q1-K1-D1	131382	BLASTX	219	2.00E-30	64	OXYGEN-EVOLVING ENHANCER PROTEIN 1 PRECURSOR (OEE1) >gi 81252 pir S05508 photosystem II oxygen-evolving complex protein 1 precursor - Chlamydomonas reinhardtii >gi 18160 emb CAA32053.1 (X13826) OEE1 precursor protein [Chlamydomonas reinhardtii] >gi 2286
1277	LIB3602-019-Q6-K1-A7	1657621	BLASTX	523	3.00E-53	64	(U72505) G6p [Arabidopsis thaliana] >gi 3068711 gb AAC14411.1 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi 5478795 dbj BAA82478.1 (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]
1278	LIB3602-019-Q6-K1-A1	1657621	BLASTX	509	1.00E-51	64	(U72505) G6p [Arabidopsis thaliana] >gi 3068711 gb AAC14411.1 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi 5478795 dbj BAA82478.1 (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]
1279	LIB3602-074-Q1-K1-A1	1657621	BLASTX	318	4.00E-29	64	(U72505) G6p [Arabidopsis thaliana] >gi 3068711 gb AAC14411.1 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi 5478795 dbj BAA82478.1 (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]
1280	LIB3602-087-Q6-K1-D2	1657621	BLASTX	293	4.00E-26	60	(U72505) G6p [Arabidopsis thaliana] >gi 3068711 gb AAC14411.1 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi 5478795 dbj BAA82478.1 (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]
1281	LIB3602-040-Q6-K1-E4	1657621	BLASTX	203	1.00E-15	68	(U72505) G6p [Arabidopsis thaliana] >gi 3068711 gb AAC14411.1 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi 5478795 dbj BAA82478.1 (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]
1282	LIB3602-071-Q1-K1-C3	1172635	BLASTX	799	4.00E-90	90	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi 7435744 pir T03776 tat binding protein homolog - rice >gi 556558 dbj BAA04615.1 (D17789) rice homologue of Tat binding protein [Oryza sativa]
1283	LIB3602-049-Q6-K1-A5	1172635	BLASTX	744	5.00E-79	86	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi 7435744 pir T03776 tat binding protein homolog - rice >gi 556558 dbj BAA04615.1 (D17789) rice homologue of Tat binding protein [Oryza sativa]
1284	LIB3602-049-Q6-K1-A6	1172635	BLASTX	719	4.00E-76	84	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi 7435744 pir T03776 tat binding protein homolog - rice >gi 556558 dbj BAA04615.1 (D17789) rice homologue of Tat binding protein [Oryza sativa]
1285	LIB3602-106-Q1-K1-H10	1172635	BLASTX	467	1.00E-46	72	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi 7435744 pir T03776 tat binding

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1286	LIB3602-013-Q6-K1-C6	1172635	BLASTX	246	5.00E-25	66	protein homolog - rice >gi 556558 dbj BAA04615.1 (D17789) rice homologue of Tat binding protein [Oryza sativa] 26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi 7435744 pir T03776 tat binding protein homolog - rice >gi 556558 dbj BAA04615.1 (D17789) rice homologue of Tat binding protein [Oryza sativa]
1287	LIB3602-114-Q1-K1-F1	131772	BLASTX	595	1.00E-61	85	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) - maize
1288	LIB3602-039-Q6-K1-F12	131772	BLASTX	595	1.00E-61	85	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) - maize
1289	LIB3602-034-Q6-K1-F7	131772	BLASTX	488	3.00E-49	91	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) - maize
1290	LIB3602-059-Q6-K1-H5	131772	BLASTX	485	1.00E-48	90	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) - maize
1291	LIB3602-035-Q1-K1-F7	131772	BLASTX	460	1.00E-45	91	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) >gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) - maize
1292	LIB3602-053-Q6-K1-C3	4757371	BLASTX	272	1.00E-23	76	(AB026686) chlorophyll a/b-binding protein precursor [Physcomitrella patens]
1293	LIB3602-102-Q1-K1-G9	4757371	BLASTX	268	3.00E-23	85	(AB026686) chlorophyll a/b-binding protein precursor [Physcomitrella patens]
1294	LIB3602-070-Q1-K1-B10	4757371	BLASTX	268	3.00E-23	85	(AB026686) chlorophyll a/b-binding protein precursor [Physcomitrella patens]
1295	LIB3602-102-Q1-K1-G10	4757371	BLASTX	188	6.00E-14	84	(AB026686) chlorophyll a/b-binding protein precursor [Physcomitrella patens]
1296	LIB3602-084-Q6-K1-C12	4757371	BLASTX	161	6.00E-11	69	(AB026686) chlorophyll a/b-binding protein precursor [Physcomitrella patens]
1297	LIB3602-002-P1-K6-A7	6015604	BLASTX	466	1.00E-48	62	(X97322) ribosomal protein L9 [Pisum sativum]
1298	LIB3602-052-Q6-K1-F7	6015604	BLASTX	409	7.00E-40	58	(X97322) ribosomal protein L9 [Pisum sativum]
1299	LIB3602-056-Q6-K1-C10	6015604	BLASTX	399	1.00E-38	58	(X97322) ribosomal protein L9 [Pisum sativum]
1300	LIB3602-020-Q6-K1-F9	6015604	BLASTX	319	2.00E-29	60	(X97322) ribosomal protein L9 [Pisum sativum]
1301	LIB3602-038-Q6-K1-G9	6015604	BLASTX	312	1.00E-28	59	(X97322) ribosomal protein L9 [Pisum sativum]
1302	LIB3602-069-Q1-K1-F5	7109466	BLASTX	481	4.00E-48	57	(AC016662) putative 60S ribosomal protein L6 [Arabidopsis thaliana]
1303	LIB3602-092-Q6-K6-H4	7109466	BLASTX	453	8.00E-45	61	(AC016662) putative 60S ribosomal protein L6 [Arabidopsis thaliana]
1304	LIB3602-027-Q6-K1-B9	7109466	BLASTX	443	9.00E-44	58	(AC016662) putative 60S ribosomal protein L6 [Arabidopsis thaliana]
1305	LIB3602-047-Q6-K1-C9	7109466	BLASTX	432	2.00E-42	66	(AC016662) putative 60S ribosomal protein L6 [Arabidopsis thaliana]
1306	LIB3602-046-Q6-K1-C9	7109466	BLASTX	409	7.00E-40	60	(AC016662) putative 60S ribosomal protein L6 [Arabidopsis thaliana]
1307	LIB3602-030-Q6-K1-E2	6225817	BLASTX	507	2.00E-51	66	DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [INCLUDES: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1308	LIB3602-030-Q6-K1-B9	6225817	BLASTX	500	2.00E-50	65	>gi 7488983 pir T DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [INCLUDES: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)]
1309	LIB3602-101-Q1-K1-E10	6225817	BLASTX	351	4.00E-37	77	>gi 7488983 pir T DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [INCLUDES: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)]
1310	LIB3602-048-Q6-K1QA-B4	6225817	BLASTX	289	1.00E-36	67	>gi 7488983 pir T DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [INCLUDES: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)]
1311	LIB3602-087-Q6-K1-D12	6225817	BLASTX	348	1.00E-33	71	>gi 7488983 pir T DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (P5CS) [INCLUDES: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)]
1312	LIB3602-058-Q6-K1-C6	7019398	BLASTN	37	5.00E-11	100	>gi 7488983 pir T Homo sapiens gonadotropin-regulated testicular RNA helicase (GRTH), mRNA
1313	LIB3602-077-Q6-K6-C7	7019398	BLASTN	36	7.00E-11	100	Homo sapiens gonadotropin-regulated testicular RNA helicase (GRTH), mRNA
1314	LIB3602-040-Q6-K1-A11	7019398	BLASTN	36	2.00E-10	100	Homo sapiens gonadotropin-regulated testicular RNA helicase (GRTH), mRNA
1315	LIB3602-079-Q6-K6-A4	7019398	BLASTN	36	2.00E-10	100	Homo sapiens gonadotropin-regulated testicular RNA helicase (GRTH), mRNA
1316	LIB3602-118-Q1-K1-B10	7019398	BLASTN	36	2.00E-10	100	Homo sapiens gonadotropin-regulated testicular RNA helicase (GRTH), mRNA
1317	LIB3602-069-Q1-K1-F2	4581162	BLASTX	499	3.00E-50	78	(AC006220) putative microtubule-associated protein [Arabidopsis thaliana]
1318	LIB3602-068-Q1-K1-F2	4581162	BLASTX	499	3.00E-50	78	(AC006220) putative microtubule-associated protein [Arabidopsis thaliana]
1319	LIB3602-039-Q6-K1-E5	4581162	BLASTX	499	3.00E-50	78	(AC006220) putative microtubule-associated protein [Arabidopsis thaliana]
1320	LIB3602-047-Q6-K1-F7	4581162	BLASTX	476	1.00E-47	77	(AC006220) putative microtubule-associated protein [Arabidopsis thaliana]
1321	LIB3602-086-Q6-K1-F1	4581162	BLASTX	353	3.00E-33	58	(AC006220) putative microtubule-associated protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1322	LIB3602-045-Q6-K1-B9	968987	BLASTX	232	4.00E-19	52	(U31648) ferritin [Glycine max]
1323	LIB3602-102-Q1-K1-A4	968987	BLASTX	229	1.00E-18	51	(U31648) ferritin [Glycine max]
1324	LIB3602-105-Q1-K1-G6	968987	BLASTX	218	2.00E-17	54	(U31648) ferritin [Glycine max]
1325	LIB3602-067-Q1-K1-A11	968987	BLASTX	218	2.00E-17	54	(U31648) ferritin [Glycine max]
1326	LIB3602-070-Q1-K1-H9	968987	BLASTX	201	2.00E-15	52	(U31648) ferritin [Glycine max]
1327	LIB3602-095-Q6-K6-H11	4966342	BLASTX	224	5.00E-18	46	(AC006341) ESTs gb T04357 and gb AA595092 come from this gene. [Arabidopsis thaliana]
1328	LIB3602-079-Q6-K6-C9	4966342	BLASTX	224	5.00E-18	46	(AC006341) ESTs gb T04357 and gb AA595092 come from this gene. [Arabidopsis thaliana]
1329	LIB3602-116-Q1-K1-H11	4966342	BLASTX	224	6.00E-18	46	(AC006341) ESTs gb T04357 and gb AA595092 come from this gene. [Arabidopsis thaliana]
1330	LIB3602-112-Q1-K1-H11	4966342	BLASTX	207	5.00E-16	46	(AC006341) ESTs gb T04357 and gb AA595092 come from this gene. [Arabidopsis thaliana]
1331	LIB3602-089-Q6-K6-H11	4966342	BLASTX	203	1.00E-15	46	(AC006341) ESTs gb T04357 and gb AA595092 come from this gene. [Arabidopsis thaliana]
1332	LIB3602-066-Q1-K6-C9	6714454	BLASTX	336	4.00E-31	61	(AC011620) putative 60S ribosomal protein L22 [Arabidopsis thaliana]
1333	LIB3602-051-Q6-K1-D10	6714454	BLASTX	276	3.00E-24	61	(AC011620) putative 60S ribosomal protein L22 [Arabidopsis thaliana]
1334	LIB3602-008-Q6-K1-H9	6714454	BLASTX	255	8.00E-22	60	(AC011620) putative 60S ribosomal protein L22 [Arabidopsis thaliana]
1335	LIB3602-103-Q1-K1-F5	6714454	BLASTX	158	8.00E-14	54	(AC011620) putative 60S ribosomal protein L22 [Arabidopsis thaliana]
1336	LIB3602-018-Q6-K1-A9	6714454	BLASTX	163	5.00E-11	57	(AC011620) putative 60S ribosomal protein L22 [Arabidopsis thaliana]
1337	LIB3602-066-Q1-K6-H11	1805719	BLASTX	497	4.00E-60	70	(Y10657) Rubisco activase [Chlorococccum littorale]
1338	LIB3602-106-Q1-K1-E4	1805719	BLASTX	497	4.00E-60	70	(Y10657) Rubisco activase [Chlorococccum littorale]
1339	LIB3602-029-Q6-K1-A5	1805719	BLASTX	558	3.00E-57	71	(Y10657) Rubisco activase [Chlorococccum littorale]
1340	LIB3602-040-Q6-K1-A10	1805719	BLASTX	554	6.00E-57	81	(Y10657) Rubisco activase [Chlorococccum littorale]
1341	LIB3602-041-Q6-K1-H5	1805719	BLASTX	361	3.00E-34	64	(Y10657) Rubisco activase [Chlorococccum littorale]
1342	LIB3602-048-Q6-K1QA-F3	595768	BLASTX	157	2.00E-10	66	(U13866) non-functional lacZ alpha peptide [unidentified cloning vector]
1343	LIB3602-016-Q6-K1-E12	595768	BLASTX	157	3.00E-10	65	(U13866) non-functional lacZ alpha peptide [unidentified cloning vector]
1344	LIB3602-056-Q6-K1-B5	595768	BLASTX	151	1.00E-09	63	(U13866) non-functional lacZ alpha peptide [unidentified cloning vector]
1345	LIB3602-088-Q6-K6-A11	595768	BLASTX	148	4.00E-09	56	(U13866) non-functional lacZ alpha peptide [unidentified cloning vector]
1346	LIB3602-017-Q6-K1-F3	7019661	BLASTX	318	3.00E-29	86	(AL132954) ribosomal L23a-like protein [Arabidopsis thaliana]
1347	LIB3602-115-Q1-K1-G4	7019661	BLASTX	203	9.00E-16	61	(AL132954) ribosomal L23a-like protein [Arabidopsis thaliana]
1348	LIB3602-107-Q1-K1-E9	7019661	BLASTX	172	4.00E-12	75	(AL132954) ribosomal L23a-like protein [Arabidopsis thaliana]
1349	LIB3602-067-Q1-K1-D9	7019661	BLASTX	149	2.00E-10	90	(AL132954) ribosomal L23a-like protein [Arabidopsis thaliana]
1350	LIB3602-073-Q1-K1-A7	5706704	BLASTX	341	8.00E-32	64	(AF112440) ribosomal protein S26 [Pisum sativum]
1351	LIB3602-111-Q1-K1-D1	5706704	BLASTX	236	2.00E-19	64	(AF112440) ribosomal protein S26 [Pisum sativum]
1352	LIB3602-044-Q6-K1-B5	5706704	BLASTX	231	5.00E-19	63	(AF112440) ribosomal protein S26 [Pisum sativum]
1353	LIB3602-053-Q6-K1-A7	5706704	BLASTX	152	2.00E-10	55	(AF112440) ribosomal protein S26 [Pisum sativum]
1354	LIB3602-059-Q6-K1-C4	399014	BLASTX	685	4.00E-72	74	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi 99444 pir A41677 ADP,ATP carrier protein - Chlorella kessleri >gi 516597 gb AAA33027.1 (M76669) ATP/ADP

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1355	LIB3602-050-Q6-K1-F7	399014	BLASTX	656	8.00E-69	81	translocator [Chlorella kessleri] ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi 99444 pir A41677 ADP,ATP carrier protein - Chlorella kessleri >gi 516597 gb AAA33027.1 (M76669) ATP/ADP translocator [Chlorella kessleri]
1356	LIB3602-018-Q6-K1-E11	399014	BLASTX	379	3.00E-36	72	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi 99444 pir A41677 ADP,ATP carrier protein - Chlorella kessleri >gi 516597 gb AAA33027.1 (M76669) ATP/ADP translocator [Chlorella kessleri]
1357	LIB3602-044-Q6-K1-E11	399014	BLASTX	176	1.00E-12	81	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi 99444 pir A41677 ADP,ATP carrier protein - Chlorella kessleri >gi 516597 gb AAA33027.1 (M76669) ATP/ADP translocator [Chlorella kessleri]
1358	LIB3602-067-Q1-K1-E2	7294504	BLASTX	338	1.00E-31	63	(AE003539) RpS4 gene product [alt 2] [Drosophila melanogaster] >gi 7294505 gb AAF49847.1 (AE003539) RpS4 gene product [alt 1] [Drosophila melanogaster]
1359	LIB3602-051-Q6-K1-A7	7294504	BLASTX	272	5.00E-24	69	(AE003539) RpS4 gene product [alt 2] [Drosophila melanogaster] >gi 7294505 gb AAF49847.1 (AE003539) RpS4 gene product [alt 1] [Drosophila melanogaster]
1360	LIB3602-003-Q1-K1-E9	7294504	BLASTX	261	9.00E-23	67	(AE003539) RpS4 gene product [alt 2] [Drosophila melanogaster] >gi 7294505 gb AAF49847.1 (AE003539) RpS4 gene product [alt 1] [Drosophila melanogaster]
1361	LIB3602-006-Q1-K1-E3	7294504	BLASTX	214	7.00E-21	68	(AE003539) RpS4 gene product [alt 2] [Drosophila melanogaster] >gi 7294505 gb AAF49847.1 (AE003539) RpS4 gene product [alt 1] [Drosophila melanogaster]
1362	LIB3602-054-Q6-K1-C12	7440943	BLASTX	498	3.00E-50	72	ribosomal protein L19.T2H3.3 - Arabidopsis thaliana >gi 3377797 gb AAC28170.1 (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A
1363	LIB3602-043-Q6-K1-E10	7440943	BLASTX	341	6.00E-32	68	ribosomal protein L19.T2H3.3 - Arabidopsis thaliana >gi 3377797 gb AAC28170.1 (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A
1364	LIB3602-044-Q6-K1-H8	7440943	BLASTX	251	2.00E-21	63	ribosomal protein L19.T2H3.3 - Arabidopsis thaliana >gi 3377797 gb AAC28170.1 (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A
1365	LIB3602-039-Q6-K1-B8	7440943	BLASTX	190	3.00E-14	75	ribosomal protein L19.T2H3.3 - Arabidopsis thaliana >gi 3377797 gb AAC28170.1 (AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1366	LIB3602-022-Q6-K1-E8	7433282	BLASTX	575	2.00E-59	74	cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii >gi 2696717 dbj BAA23881.1 (AB007640) chloroplast w6 desaturase [Chlamydomonas reinhardtii]
1367	LIB3602-012-Q6-K1-F3	7433282	BLASTX	394	4.00E-38	68	omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii >gi 2696717 dbj BAA23881.1 (AB007640) chloroplast w6 desaturase [Chlamydomonas reinhardtii]
1368	LIB3602-016-Q6-K1-D3	7433282	BLASTX	151	7.00E-10	59	omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii >gi 2696717 dbj BAA23881.1 (AB007640) chloroplast w6 desaturase [Chlamydomonas reinhardtii]
1369	LIB3602-053-Q6-K1-B7	7433282	BLASTX	151	1.00E-09	59	omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii >gi 2696717 dbj BAA23881.1 (AB007640) chloroplast w6 desaturase [Chlamydomonas reinhardtii]
1370	LIB3602-083-Q6-K6-C6	7484374	BLASTX	433	2.00E-42	51	envelope protein LIP-36G1, low CO2 inducible - Chlamydomonas reinhardtii >gi 2459573 gb AAB71743.1 (U75345) envelope protein [Chlamydomonas reinhardtii]
1371	LIB3602-118-Q1-K1-D1	7484374	BLASTX	334	4.00E-40	68	envelope protein LIP-36G1, low CO2 inducible - Chlamydomonas reinhardtii >gi 2459573 gb AAB71743.1 (U75345) envelope protein [Chlamydomonas reinhardtii]
1372	LIB3602-109-Q1-K1-C6	7484374	BLASTX	393	7.00E-38	50	envelope protein LIP-36G1, low CO2 inducible - Chlamydomonas reinhardtii >gi 2459573 gb AAB71743.1 (U75345) envelope protein [Chlamydomonas reinhardtii]
1373	LIB3602-064-Q1-K6-F7	7484374	BLASTX	153	6.00E-10	42	envelope protein LIP-36G1, low CO2 inducible - Chlamydomonas reinhardtii >gi 2459573 gb AAB71743.1 (U75345) envelope protein [Chlamydomonas reinhardtii]
1374	LIB3602-112-Q1-K1-G4	3776572	BLASTX	307	9.00E-28	38	(AC005388) ESTs gb R65052, gb AA712146, gb H76533, gb H76282, gb AA650771, gb H76287, gb AA650887, gb N37383, gb Z29721 and gb Z29722 come from this gene. [Arabidopsis thaliana]
1375	LIB3602-032-Q6-K1-G3	3776572	BLASTX	188	6.00E-14	38	(AC005388) ESTs gb R65052, gb AA712146, gb H76533, gb H76282, gb AA650771, gb H76287, gb AA650887, gb N37383, gb Z29721 and gb Z29722 come from this gene. [Arabidopsis thaliana]
1376	LIB3602-032-Q6-K1-F12	3776572	BLASTX	187	8.00E-14	39	(AC005388) ESTs gb R65052, gb AA712146, gb H76533, gb H76282, gb AA650771, gb H76287, gb AA650887, gb N37383, gb Z29721 and gb Z29722 come from this gene. [Arabidopsis thaliana]
1377	LIB3602-044-Q6-K1-E4	3776572	BLASTX	185	1.00E-13	39	(AC005388) ESTs gb R65052, gb AA712146, gb H76533, gb H76282, gb AA650771, gb H76287, gb AA650887, gb N37383, gb Z29721 and gb Z29722 come from this gene. [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1378	LIB3602-027-Q6-K1-C9	2492870	BLASTX	474	2.00E-47	52	SERINE--GLYOXYLATE AMINOTRANSFERASE (SGAT)
1379	LIB3602-046-Q6-K1-F9	2492870	BLASTX	422	2.00E-41	51	SERINE--GLYOXYLATE AMINOTRANSFERASE (SGAT)
1380	LIB3602-013-Q6-K1-B5	2492870	BLASTX	419	5.00E-41	51	SERINE--GLYOXYLATE AMINOTRANSFERASE (SGAT)
1381	LIB3602-045-Q6-K1-D2	2492870	BLASTX	259	3.00E-22	50	SERINE--GLYOXYLATE AMINOTRANSFERASE (SGAT)
1382	LIB3602-076-Q6-K6-G4	6513924	BLASTX	182	3.00E-20	42	(AC011664) putative 40S ribosomal protein S19 [Arabidopsis thaliana]
1383	LIB3602-085-Q6-K1-E2	6513924	BLASTX	200	3.00E-15	35	(AC011664) putative 40S ribosomal protein S19 [Arabidopsis thaliana]
1384	LIB3602-077-Q6-K6-G2	6513924	BLASTX	146	4.00E-09	55	(AC011664) putative 40S ribosomal protein S19 [Arabidopsis thaliana]
1385	LIB3602-065-Q1-K6-C7	6513924	BLASTX	146	4.00E-09	55	(AC011664) putative 40S ribosomal protein S19 [Arabidopsis thaliana]
1386	LIB3602-113-Q1-K1-A2	4406134	BLASTX	320	2.00E-29	62	(AF083392) promoter active fragment E3 [Synechococcus PCC7942]
1387	LIB3602-112-Q1-K1-A2	4406134	BLASTX	320	3.00E-29	62	(AF083392) promoter active fragment E3 [Synechococcus PCC7942]
1388	LIB3602-093-Q6-K6-A6	4406134	BLASTX	320	3.00E-29	62	(AF083392) promoter active fragment E3 [Synechococcus PCC7942]
1389	LIB3602-044-Q6-K1-B9	4406134	BLASTX	272	9.00E-24	66	(AF083392) promoter active fragment E3 [Synechococcus PCC7942]
1390	LIB3602-007-Q1-K1-F9	7448603	BLASTX	650	7.00E-68	53	flavoprotein, 63.5K - Synechocystis sp. (strain PCC 6803) >gi 1001242 dbj BAA10483.1 (D64003) flavoprotein [Synechocystis sp.]
1391	LIB3602-072-Q1-K1-G1	7448603	BLASTX	504	8.00E-51	59	flavoprotein, 63.5K - Synechocystis sp. (strain PCC 6803) >gi 1001242 dbj BAA10483.1 (D64003) flavoprotein [Synechocystis sp.]
1392	LIB3602-004-Q1-K1-G7	7448603	BLASTX	226	2.00E-18	57	flavoprotein, 63.5K - Synechocystis sp. (strain PCC 6803) >gi 1001242 dbj BAA10483.1 (D64003) flavoprotein [Synechocystis sp.]
1393	LIB3602-107-Q1-K1-B1	7448603	BLASTX	141	2.00E-14	65	flavoprotein, 63.5K - Synechocystis sp. (strain PCC 6803) >gi 1001242 dbj BAA10483.1 (D64003) flavoprotein [Synechocystis sp.]
1394	LIB3602-090-Q6-K6-B12	2290991	BLASTX	425	1.00E-41	57	(AF006000) unknown [Bordetella pertussis]
1395	LIB3602-091-Q6-K6-B12	2290991	BLASTX	425	1.00E-41	57	(AF006000) unknown [Bordetella pertussis]
1396	LIB3602-094-Q6-K6-B12	2290991	BLASTX	347	6.00E-34	55	(AF006000) unknown [Bordetella pertussis]
1397	LIB3602-039-Q6-K1-D1	2290991	BLASTX	297	1.00E-26	55	(AF006000) unknown [Bordetella pertussis]
1398	LIB3602-074-Q1-K1-A5	6714451	BLASTX	319	1.00E-37	80	(AC011620) putative 60S ribosomal protein L18 [Arabidopsis thaliana]
1399	LIB3602-037-Q6-K1-F9	6714451	BLASTX	370	2.00E-35	78	(AC011620) putative 60S ribosomal protein L18 [Arabidopsis thaliana]
1400	LIB3602-069-Q1-K1-D4	6714451	BLASTX	308	2.00E-28	81	(AC011620) putative 60S ribosomal protein L18 [Arabidopsis thaliana]
1401	LIB3602-086-Q6-K1-B2	6714451	BLASTX	163	3.00E-11	85	(AC011620) putative 60S ribosomal protein L18 [Arabidopsis thaliana]
1402	LIB3602-056-Q6-K1-B11	3851636	BLASTX	482	2.00E-48	60	(AF098519) unknown [Avicennia marina] >gi 4128206 gb AAD03501.1 (AF056316) 40S ribosome protein S7 [Avicennia marina]
1403	LIB3602-047-Q6-K1-D3	3851636	BLASTX	300	3.00E-27	67	(AF098519) unknown [Avicennia marina] >gi 4128206 gb AAD03501.1 (AF056316) 40S ribosome protein S7 [Avicennia marina]
1404	LIB3602-084-Q6-K1-A1	3851636	BLASTX	192	2.00E-14	40	(AF098519) unknown [Avicennia marina] >gi 4128206 gb AAD03501.1 (AF056316) 40S ribosome protein S7 [Avicennia marina]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1405	LIB3602-091-Q6-K6-B3	3851636	BLASTX	146	3.00E-14	62	(AF098519) unknown [Avicennia marina] >gi 4128206 gb AAD03501.1 (AF056316) 40S ribosome protein S7 [Avicennia marina]
1406	LIB3602-071-Q1-K1-D7	4836876	BLASTX	565	5.00E-58	66	(AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana]
1407	LIB3602-010-Q6-K1-B3	4836876	BLASTX	441	2.00E-43	57	(AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana]
1408	LIB3602-037-Q6-K1-F10	4836876	BLASTX	334	6.00E-31	52	(AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana]
1409	LIB3602-057-Q6-K1-A3	4836876	BLASTX	170	2.00E-24	52	(AC007260) Similar to dTDP-D-glucose 4,6-dehydratase [Arabidopsis thaliana]
1410	LIB3602-062-Q6-K1-D10	5902590	BLASTX	577	2.00E-59	69	(AF110783) rieske iron-sulfur protein precursor [Volvox carteri f. nagariensis]
1411	LIB3602-013-Q6-K1-D4	5902590	BLASTX	540	3.00E-55	77	(AF110783) rieske iron-sulfur protein precursor [Volvox carteri f. nagariensis]
1412	LIB3602-008-Q6-K1-B11	5902590	BLASTX	458	2.00E-45	81	(AF110783) rieske iron-sulfur protein precursor [Volvox carteri f. nagariensis]
1413	LIB3602-008-Q6-K1-H6	5902590	BLASTX	378	4.00E-36	57	(AF110783) rieske iron-sulfur protein precursor [Volvox carteri f. nagariensis]
1414	LIB3602-050-Q6-K1-B2	7488227	BLASTX	566	3.00E-58	74	prohibitin-like protein F20O9.200 - Arabidopsis thaliana >gi 2842494 emb CAA16891.1 (AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi 4097688 gb AAD00155.1 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi 4097694 gb AAD00158.1 (U66594) proh
1415	LIB3602-011-Q6-K1-F1	7488227	BLASTX	483	2.00E-48	71	prohibitin-like protein F20O9.200 - Arabidopsis thaliana >gi 2842494 emb CAA16891.1 (AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi 4097688 gb AAD00155.1 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi 4097694 gb AAD00158.1 (U66594) proh
1416	LIB3602-086-Q6-K1-G3	7488227	BLASTX	451	1.00E-44	70	prohibitin-like protein F20O9.200 - Arabidopsis thaliana >gi 2842494 emb CAA16891.1 (AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi 4097688 gb AAD00155.1 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi 4097694 gb AAD00158.1 (U66594) proh
1417	LIB3602-013-Q6-K1-B6	7488227	BLASTX	398	2.00E-38	73	prohibitin-like protein F20O9.200 - Arabidopsis thaliana >gi 2842494 emb CAA16891.1 (AL021749) prohibitin-like protein [Arabidopsis thaliana] >gi 4097688 gb AAD00155.1 (U66591) prohibitin 1 [Arabidopsis thaliana] >gi 4097694 gb AAD00158.1 (U66594) proh
1418	LIB3602-005-Q1-K1-F3	7484402	BLASTX	398	2.00E-38	68	protochlorophyllide reductase (EC 1.3.1.33) precursor - Chlamydomonas reinhardtii >gi 1408176 gb AAB04951.1 (U36752) NADPH:protochlorophyllide oxidoreductase [Chlamydomonas reinhardtii]
1419	LIB3602-085-Q6-K1-C11	7484402	BLASTX	387	4.00E-37	66	protochlorophyllide reductase (EC 1.3.1.33) precursor - Chlamydomonas reinhardtii >gi 1408176 gb AAB04951.1 (U36752) NADPH:protochlorophyllide oxidoreductase [Chlamydomonas reinhardtii]
1420	LIB3602-112-Q1-K1-F1	7484402	BLASTX	222	6.00E-18	61	protochlorophyllide reductase (EC 1.3.1.33) precursor - Chlamydomonas reinhardtii >gi 1408176 gb AAB04951.1 (U36752) NADPH:protochlorophyllide oxidoreductase [Chlamydomonas reinhardtii]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1421	LIB3602-093-Q6-K6-C7	7484402	BLASTX	222	6.00E-18	61	protochlorophyllide reductase (EC 1.3.1.33) precursor - Chlamydomonas reinhardtii >gi 1408176 gb AAB04951.1 (U36752) NADPH:protochlorophyllide oxidoreductase [Chlamydomonas reinhardtii]
1422	LIB3602-050-Q6-K1-D11	7488810	BLASTX	276	3.00E-24	47	hydroxyproline-rich glycoprotein 1 - garden pea (fragment) >gi 1711036 gb AAB97098.1 (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]
1423	LIB3602-058-Q6-K1-B3	7488810	BLASTX	224	4.00E-18	40	hydroxyproline-rich glycoprotein 1 - garden pea (fragment) >gi 1711036 gb AAB97098.1 (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]
1424	LIB3602-055-Q6-K1-C6	7488810	BLASTX	224	4.00E-18	40	hydroxyproline-rich glycoprotein 1 - garden pea (fragment) >gi 1711036 gb AAB97098.1 (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]
1425	LIB3602-067-Q1-K1-E10	7488810	BLASTX	217	3.00E-17	39	hydroxyproline-rich glycoprotein 1 - garden pea (fragment) >gi 1711036 gb AAB97098.1 (U78952) hydroxyproline rich glycoprotein PsHRGP1 [Pisum sativum]
1426	LIB3602-091-Q6-K6-E10	3914425	BLASTX	696	2.00E-73	73	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi 2511596 emb CAA74029.1 (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi 3421
1427	LIB3602-073-Q1-K1-E1	3914425	BLASTX	560	2.00E-57	71	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi 2511596 emb CAA74029.1 (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi 3421
1428	LIB3602-102-Q1-K1-D3	3914425	BLASTX	560	2.00E-57	71	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi 2511596 emb CAA74029.1 (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi 3421
1429	LIB3602-057-Q6-K1-D11	3914425	BLASTX	251	5.00E-37	69	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi 2511596 emb CAA74029.1 (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi 3421
1430	LIB3602-050-Q6-K1-E4	131220	BLASTX	249	4.00E-21	48	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 8.4 KD PROTEIN) (PSI-K) (P37 PROTEIN) >gi 81243 pir S06684 photosystem I 8.4K protein precursor -

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1431	LIB3602-050-Q6-K1-E3	131220	BLASTX	248	6.00E-21	60	Chlamydomonas reinhardtii >gi 81249 pir JQ0372 photosystem I protein P37 - Ch PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT- HARVESTING COMPLEX I 8.4 KD PROTEIN) (PSI-K) (P37 PROTEIN) >gi 81243 pir S06684 photosystem I 8.4K protein precursor - Chlamydomonas reinhardtii >gi 81249 pir JQ0372 photosystem I protein P37 - Ch
1432	LIB3602-011-Q6-K1-H6	131220	BLASTX	237	1.00E-19	58	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT- HARVESTING COMPLEX I 8.4 KD PROTEIN) (PSI-K) (P37 PROTEIN) >gi 81243 pir S06684 photosystem I 8.4K protein precursor - Chlamydomonas reinhardtii >gi 81249 pir JQ0372 photosystem I protein P37 - Ch
1433	LIB3602-053-Q6-K1-G4	131220	BLASTX	202	8.00E-16	62	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT- HARVESTING COMPLEX I 8.4 KD PROTEIN) (PSI-K) (P37 PROTEIN) >gi 81243 pir S06684 photosystem I 8.4K protein precursor - Chlamydomonas reinhardtii >gi 81249 pir JQ0372 photosystem I protein P37 - Ch
1434	LIB3602-003-Q1-K1-F1	7211992	BLASTX	537	7.00E-55	68	(AC004809) Strong simialrity to the disulfide isomerase precursor homolog T21L14.14 gi 2702281 from A. thaliana on BAC gb AC003033. [Arabidopsis thaliana]
1435	LIB3602-018-Q6-K1-G7	7211992	BLASTX	354	3.00E-33	48	(AC004809) Strong simialrity to the disulfide isomerase precursor homolog T21L14.14 gi 2702281 from A. thaliana on BAC gb AC003033. [Arabidopsis thaliana]
1436	LIB3602-063-Q1-K6-D12	7211992	BLASTX	344	4.00E-32	44	(AC004809) Strong simialrity to the disulfide isomerase precursor homolog T21L14.14 gi 2702281 from A. thaliana on BAC gb AC003033. [Arabidopsis thaliana]
1437	LIB3602-052-Q6-K1-C2	7211992	BLASTX	322	1.00E-29	48	(AC004809) Strong simialrity to the disulfide isomerase precursor homolog T21L14.14 gi 2702281 from A. thaliana on BAC gb AC003033. [Arabidopsis thaliana]
1438	LIB3602-115-Q1-K1-C12	2754849	BLASTX	565	5.00E-58	61	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]
1439	LIB3602-088-Q6-K6-C12	2754849	BLASTX	559	3.00E-57	59	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]
1440	LIB3602-104-Q1-K1-F7	2754849	BLASTX	557	5.00E-57	62	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]
1441	LIB3602-049-Q6-K1-G1	2754849	BLASTX	152	2.00E-12	39	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]
1442	LIB3602-035-Q1-K1-B2	2582351	BLASTX	473	3.00E-47	56	(AF018639) unknown [Dictyostelium discoideum]
1443	LIB3602-034-Q6-K1-B2	2582351	BLASTX	456	3.00E-45	57	(AF018639) unknown [Dictyostelium discoideum]
1444	LIB3602-008-Q6-K1-B1	2582351	BLASTX	277	2.00E-24	53	(AF018639) unknown [Dictyostelium discoideum]
1445	LIB3602-008-Q6-K1-D5	2582351	BLASTX	212	9.00E-17	50	(AF018639) unknown [Dictyostelium discoideum]
1446	LIB3602-113-Q1-K1-A1	3914473	BLASTX	456	2.00E-45	64	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI- L) >gi 479684 pir S35151 photosystem I chain XI precursor - spinach >gi 396275 emb CAA45775.1 (X64445) subunit XI of photosystem I reaction center [Spinacia oleracea]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1447	LIB3602-115-Q1-K1-F8	3914473	BLASTX	404	4.00E-39	59	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi 479684 pir S35151 photosystem I chain XI precursor - spinach >gi 396275 emb CAA45775.1 (X64445) subunit XI of photosystem I reaction center [Spinacia oleracea]
1448	LIB3602-106-Q1-K1-G12	3914473	BLASTX	372	2.00E-35	59	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi 479684 pir S35151 photosystem I chain XI precursor - spinach >gi 396275 emb CAA45775.1 (X64445) subunit XI of photosystem I reaction center [Spinacia oleracea]
1449	LIB3602-019-Q6-K1-A5	3914473	BLASTX	324	5.00E-30	84	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi 479684 pir S35151 photosystem I chain XI precursor - spinach >gi 396275 emb CAA45775.1 (X64445) subunit XI of photosystem I reaction center [Spinacia oleracea]
1450	LIB3602-034-Q6-K1-C8	1172816	BLASTX	647	1.00E-67	80	60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395.1 (X81799) ribosomal protein L16 [Arabidopsis thaliana]
1451	LIB3602-079-Q6-K6-D10	1172816	BLASTX	613	1.00E-63	79	60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395.1 (X81799) ribosomal protein L16 [Arabidopsis thaliana]
1452	LIB3602-077-Q6-K6-E5	1172816	BLASTX	613	1.00E-63	79	60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395.1 (X81799) ribosomal protein L16 [Arabidopsis thaliana]
1453	LIB3602-035-Q1-K1-C8	1172816	BLASTX	613	1.00E-63	79	60S RIBOSOMAL PROTEIN L11A (L16A) >gi 624938 emb CAA57395.1 (X81799) ribosomal protein L16 [Arabidopsis thaliana]
1454	LIB3602-035-Q1-K1-H8	3747050	BLASTX	435	9.00E-43	83	(AF093540) ribosomal protein L26 [Zea mays]
1455	LIB3602-064-Q1-K6-C4	3747050	BLASTX	425	1.00E-41	83	(AF093540) ribosomal protein L26 [Zea mays]
1456	LIB3602-036-Q6-K1-B6	3747050	BLASTX	256	1.00E-21	85	(AF093540) ribosomal protein L26 [Zea mays]
1457	LIB3602-034-Q6-K1-H8	3747050	BLASTX	244	3.00E-21	81	(AF093540) ribosomal protein L26 [Zea mays]
1458	LIB3602-112-Q1-K1-G6	118241	BLASTX	327	4.00E-30	49	DIHYDRODIPICOLINATE SYNTHASE PRECURSOR (DHDPS)
1459	LIB3602-092-Q6-K6-G11	118241	BLASTX	327	4.00E-30	49	DIHYDRODIPICOLINATE SYNTHASE PRECURSOR (DHDPS)
1460	LIB3602-029-Q6-K1-D5	118241	BLASTX	295	2.00E-26	55	DIHYDRODIPICOLINATE SYNTHASE PRECURSOR (DHDPS)
1461	LIB3602-028-Q6-K1-C9	118241	BLASTX	279	1.00E-24	55	DIHYDRODIPICOLINATE SYNTHASE PRECURSOR (DHDPS)
1462	LIB3602-076-Q6-K6-B11	7239379	BLASTX	647	6.00E-73	72	(AF234984) putative pseudouridine synthase [Arabidopsis thaliana]
1463	LIB3602-070-Q1-K1-A4	7239379	BLASTX	653	2.00E-68	66	(AF234984) putative pseudouridine synthase [Arabidopsis thaliana]
1464	LIB3602-074-Q1-K1-C7	7239379	BLASTX	577	2.00E-59	73	(AF234984) putative pseudouridine synthase [Arabidopsis thaliana]
1465	LIB3602-105-Q1-K1-B9	7239379	BLASTX	349	5.00E-53	72	(AF234984) putative pseudouridine synthase [Arabidopsis thaliana]
1466	LIB3602-067-Q1-K1-A3	6093871	BLASTX	724	1.00E-76	74	60S RIBOSOMAL PROTEIN L15-1 >gi 2982249 gb AAC32112.1 (AF051207) probable 60S ribosomal protein L15 [Picea mariana]
1467	LIB3602-028-Q6-K1-B1	6093871	BLASTX	676	4.00E-71	72	60S RIBOSOMAL PROTEIN L15-1 >gi 2982249 gb AAC32112.1 (AF051207) probable 60S ribosomal protein L15 [Picea mariana]
1468	LIB3602-044-Q6-K1-A9	6093871	BLASTX	621	1.00E-64	73	60S RIBOSOMAL PROTEIN L15-1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1469	LIB3602-015-Q6-K1-A9	6093871	BLASTX	346	4.00E-40	58	>gi 2982249 gb AAC32112.1 (AF051207) probable 60S ribosomal protein L15 [Picea mariana] 60S RIBOSOMAL PROTEIN L15-1
1470	LIB3602-030-Q6-K1-G7	115828	BLASTX	438	3.00E-43	76	>gi 2982249 gb AAC32112.1 (AF051207) probable 60S ribosomal protein L15 [Picea mariana] CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 81223 pir JS0172 chlorophyll a/b-binding protein precursor - green alga (Dunaliella salina) >gi 167987 gb AAA33278.1 (M23531) major chlorophyll binding protein [Dunaliella salina]
1471	LIB3602-037-Q6-K1-E7	115828	BLASTX	438	3.00E-43	76	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 81223 pir JS0172 chlorophyll a/b-binding protein precursor - green alga (Dunaliella salina) >gi 167987 gb AAA33278.1 (M23531) major chlorophyll binding protein [Dunaliella salina]
1472	LIB3602-020-Q6-K1-G11	115828	BLASTX	427	7.00E-42	76	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 81223 pir JS0172 chlorophyll a/b-binding protein precursor - green alga (Dunaliella salina) >gi 167987 gb AAA33278.1 (M23531) major chlorophyll binding protein [Dunaliella salina]
1473	LIB3602-101-Q1-K1-D10	115828	BLASTX	393	8.00E-38	75	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 81223 pir JS0172 chlorophyll a/b-binding protein precursor - green alga (Dunaliella salina) >gi 167987 gb AAA33278.1 (M23531) major chlorophyll binding protein [Dunaliella salina]
1474	LIB3602-012-Q6-K1-D1	115770	BLASTX	672	2.00E-70	79	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 100533 pir S07448 chlorophyll a/b-binding protein - swollen duckweed >gi 168290 gb AAA33392.1 (M12152) chlorophyll a/b apoprotein [Lemna gibba]
1475	LIB3602-086-Q6-K1-A11	115770	BLASTX	544	8.00E-70	81	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 100533 pir S07448 chlorophyll a/b-binding protein - swollen duckweed >gi 168290 gb AAA33392.1 (M12152) chlorophyll a/b apoprotein [Lemna gibba]
1476	LIB3602-018-Q6-K1-C8	115770	BLASTX	650	5.00E-68	78	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 100533 pir S07448 chlorophyll a/b-binding protein - swollen duckweed >gi 168290 gb AAA33392.1 (M12152) chlorophyll a/b apoprotein [Lemna gibba]
1477	LIB3602-048-Q6-K1QA-E1	115770	BLASTX	606	7.00E-63	73	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 100533 pir S07448 chlorophyll a/b-binding protein - swollen duckweed >gi 168290 gb AAA33392.1 (M12152) chlorophyll a/b apoprotein [Lemna gibba]
1478	LIB3602-048-Q6-K1QA-C9	6682246	BLASTX	404	3.00E-39	93	(AC016661) putative 40S ribosomal protein S23 [Arabidopsis thaliana]
1479	LIB3602-101-Q1-K1-F10	6682246	BLASTX	347	1.00E-32	91	(AC016661) putative 40S ribosomal protein S23 [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1480	LIB3602-077-Q6-K6-A4	6682246	BLASTX	284	2.00E-25	91	(AC016661) putative 40S ribosomal protein S23 [Arabidopsis thaliana]
1481	LIB3602-074-Q1-K1-C5	1350995	BLASTX	714	2.00E-75	68	40S RIBOSOMAL PROTEIN S4 >gi 1362730 pir A56537 ribosomal protein S4, cytosolic - chicken >gi 402296 gb AAB59946.1 (L24368) ribosomal protein S4 [Gallus gallus]
1482	LIB3602-023-Q6-K1-G1	1350995	BLASTX	674	8.00E-71	70	40S RIBOSOMAL PROTEIN S4 >gi 1362730 pir A56537 ribosomal protein S4, cytosolic - chicken >gi 402296 gb AAB59946.1 (L24368) ribosomal protein S4 [Gallus gallus]
1483	LIB3602-061-Q6-K1-D8	1350995	BLASTX	535	1.00E-54	62	40S RIBOSOMAL PROTEIN S4 >gi 1362730 pir A56537 ribosomal protein S4, cytosolic - chicken >gi 402296 gb AAB59946.1 (L24368) ribosomal protein S4 [Gallus gallus]
1484	LIB3602-046-Q6-K1-H5	7485005	BLASTX	382	1.00E-36	59	helicase homolog T6H20.10 - Arabidopsis thaliana (fragment) >gi 5541663 emb CAB51169.1 (AL096859) putative helicase, fragment [Arabidopsis thaliana]
1485	LIB3602-112-Q1-K1-B9	7485005	BLASTX	319	3.00E-29	66	helicase homolog T6H20.10 - Arabidopsis thaliana (fragment) >gi 5541663 emb CAB51169.1 (AL096859) putative helicase, fragment [Arabidopsis thaliana]
1486	LIB3602-094-Q6-K6-B9	7485005	BLASTX	310	4.00E-28	64	helicase homolog T6H20.10 - Arabidopsis thaliana (fragment) >gi 5541663 emb CAB51169.1 (AL096859) putative helicase, fragment [Arabidopsis thaliana]
1487	LIB3602-076-Q6-K6-D10	6587821	BLASTX	230	6.00E-19	57	(AC010924) Contains similarity to gb AF181686 membrane protein TMS1d from Drosophila melanogaster. ESTs gb R64994, gb AI994832, gb Z47674 come from this gene. [Arabidopsis thaliana]
1488	LIB3602-070-Q1-K1-A9	6587821	BLASTX	203	1.00E-15	56	(AC010924) Contains similarity to gb AF181686 membrane protein TMS1d from Drosophila melanogaster. ESTs gb R64994, gb AI994832, gb Z47674 come from this gene. [Arabidopsis thaliana]
1489	LIB3602-010-Q6-K1-E4	6587821	BLASTX	190	3.00E-14	36	(AC010924) Contains similarity to gb AF181686 membrane protein TMS1d from Drosophila melanogaster. ESTs gb R64994, gb AI994832, gb Z47674 come from this gene. [Arabidopsis thaliana]
1490	LIB3602-116-Q1-K1-A5	4139217	BLASTN	61	9.00E-26	92	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds
1491	LIB3602-004-Q1-K1-B3	4139217	BLASTN	51	2.00E-19	92	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds
1492	LIB3602-063-Q1-K6-B8	4139217	BLASTN	42	5.00E-14	96	Chlamydomonas reinhardtii light harvesting complex II protein precursor (Lhcb3) mRNA, complete cds
1493	LIB3602-009-Q6-K1-D7	4262250	BLASTX	691	8.00E-73	78	(AC006200) putative fructose-bisphosphate aldolase, plastidic form [Arabidopsis thaliana]
1494	LIB3602-004-Q1-K1-C1	4262250	BLASTX	563	5.00E-63	73	(AC006200) putative fructose-bisphosphate aldolase, plastidic form [Arabidopsis thaliana]
1495	LIB3602-043-Q6-K1-A8	4262250	BLASTX	473	3.00E-47	72	(AC006200) putative fructose-bisphosphate aldolase, plastidic form [Arabidopsis thaliana]
1496	LIB3602-009-Q6-K1-B1	6996529	BLASTX	556	5.00E-57	71	(AJ271785) enolase [Lupinus luteus]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1497	LIB3602-037-Q6-K1-G2	6996529	BLASTX	249	4.00E-21	85	(AJ271785) enolase [<i>Lupinus luteus</i>]
1498	LIB3602-015-Q6-K1-H10	6996529	BLASTX	211	2.00E-16	89	(AJ271785) enolase [<i>Lupinus luteus</i>]
1499	LIB3602-023-Q6-K1-A3	2708624	BLASTX	615	6.00E-64	66	(AF036618) acetyl-CoA synthetase [<i>Arabidopsis thaliana</i>]
1500	LIB3602-108-Q1-K1-G5	2708624	BLASTX	595	1.00E-61	69	(AF036618) acetyl-CoA synthetase [<i>Arabidopsis thaliana</i>]
1501	LIB3602-119-Q1-K1-F11	2708624	BLASTX	166	5.00E-12	71	(AF036618) acetyl-CoA synthetase [<i>Arabidopsis thaliana</i>]
1502	LIB3602-063-Q1-K6-F4	131174	BLASTX	272	4.00E-24	77	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E) >gi 81245 pir S04134 photosystem I chain IV precursor - <i>Chlamydomonas reinhardtii</i> >gi 18180 emb CAA31850.1 (X13496) P30 precursor protein [<i>Chlamydomonas</i>]
1503	LIB3602-070-Q1-K1-E6	131174	BLASTX	268	2.00E-23	78	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E) >gi 81245 pir S04134 photosystem I chain IV precursor - <i>Chlamydomonas reinhardtii</i> >gi 18180 emb CAA31850.1 (X13496) P30 precursor protein [<i>Chlamydomonas</i>]
1504	LIB3602-021-Q6-K1-A5	131174	BLASTX	219	6.00E-18	78	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 8.1 KD PROTEIN) (P30 PROTEIN) (PSI-E) >gi 81245 pir S04134 photosystem I chain IV precursor - <i>Chlamydomonas reinhardtii</i> >gi 18180 emb CAA31850.1 (X13496) P30 precursor protein [<i>Chlamydomonas</i>]
1505	LIB3602-066-Q1-K6-D9	1345698	BLASTX	528	9.00E-54	68	CHLOROPHYLL A-B BINDING PROTEIN 151 PRECURSOR (LHCII TYPE II CAB-151) (LHCP) >gi 99601 pir S20917 chlorophyll a/b-binding protein - upland cotton >gi 452314 emb CAA38025.1 (X54090) chlorophyll ab binding protein [<i>Gossypium hirsutum</i>]
1506	LIB3602-065-Q1-K6-B9	1345698	BLASTX	418	2.00E-48	71	CHLOROPHYLL A-B BINDING PROTEIN 151 PRECURSOR (LHCII TYPE II CAB-151) (LHCP) >gi 99601 pir S20917 chlorophyll a/b-binding protein - upland cotton >gi 452314 emb CAA38025.1 (X54090) chlorophyll ab binding protein [<i>Gossypium hirsutum</i>]
1507	LIB3602-053-Q6-K1-C1	1345698	BLASTX	301	4.00E-27	78	CHLOROPHYLL A-B BINDING PROTEIN 151 PRECURSOR (LHCII TYPE II CAB-151) (LHCP) >gi 99601 pir S20917 chlorophyll a/b-binding protein - upland cotton >gi 452314 emb CAA38025.1 (X54090) chlorophyll ab binding protein [<i>Gossypium hirsutum</i>]
1508	LIB3602-069-Q1-K1-D2	7329685	BLASTX	306	1.00E-27	69	(AL162295) transketolase-like protein [<i>Arabidopsis thaliana</i>]
1509	LIB3602-086-Q6-K1-G1	7329685	BLASTX	306	1.00E-27	69	(AL162295) transketolase-like protein [<i>Arabidopsis thaliana</i>]
1510	LIB3602-026-Q6-K1-E6	7329685	BLASTX	231	6.00E-19	68	(AL162295) transketolase-like protein [<i>Arabidopsis thaliana</i>]
1511	LIB3602-010-Q6-K1-D3	115519	BLASTX	667	5.00E-70	85	CALMODULIN >gi 169306 gb AAA21424.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1512	LIB3602-039-Q6-K1-E10	115519	BLASTX	634	4.00E-66	87	(M83535) calmodulin [Phytophthora infestans] CALMODULIN >gi 169306 gb AAA21424.1
1513	LIB3602-019-Q6-K1-C5	115519	BLASTX	349	5.00E-33	84	(M83535) calmodulin [Phytophthora infestans] CALMODULIN >gi 169306 gb AAA21424.1
1514	LIB3602-004-Q1-K1-C4	100573	BLASTX	363	2.00E-34	48	(M83535) calmodulin [Phytophthora infestans] chlorophyll a/b-binding protein CP29 precursor - barley >gi 18958 emb CAA44777.1 (X63052) Precursor of CP29, core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) [Hordeum vulgare] >gi 445122 prf 1908428A chlorophyll a/b- binding protein [
1515	LIB3602-021-Q6-K1-B4	100573	BLASTX	293	1.00E-26	64	chlorophyll a/b-binding protein CP29 precursor - barley >gi 18958 emb CAA44777.1 (X63052) Precursor of CP29, core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) [Hordeum vulgare] >gi 445122 prf 1908428A chlorophyll a/b- binding protein [
1516	LIB3602-052-Q6-K1-B10	100573	BLASTX	185	6.00E-14	60	chlorophyll a/b-binding protein CP29 precursor - barley >gi 18958 emb CAA44777.1 (X63052) Precursor of CP29, core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) [Hordeum vulgare] >gi 445122 prf 1908428A chlorophyll a/b- binding protein [
1517	LIB3602-085-Q6-K1-D12	548770	BLASTX	629	1.00E-65	71	60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal protein L3.e, cytosolic - rice >gi 303853 dbj BAA02155.1 (D12630) ribosomal protein L3 [Oryza sativa]
1518	LIB3602-013-Q6-K1-B12	548770	BLASTX	607	4.00E-63	75	60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal protein L3.e, cytosolic - rice >gi 303853 dbj BAA02155.1 (D12630) ribosomal protein L3 [Oryza sativa]
1519	LIB3602-112-Q1-K1-H12	548770	BLASTX	259	3.00E-45	59	60S RIBOSOMAL PROTEIN L3 >gi 481228 pir S38359 ribosomal protein L3.e, cytosolic - rice >gi 303853 dbj BAA02155.1 (D12630) ribosomal protein L3 [Oryza sativa]
1520	LIB3602-069-Q1-K1-A12	1663720	BLASTX	528	1.00E-53	57	(U49976) beta-type carbonic anhydrase beta-CA1 [Coccomyxa sp. PA]
1521	LIB3602-068-Q1-K1-A12	1663720	BLASTX	519	1.00E-52	56	(U49976) beta-type carbonic anhydrase beta-CA1 [Coccomyxa sp. PA]
1522	LIB3602-062-Q6-K1-G1	1663720	BLASTX	216	4.00E-17	53	(U49976) beta-type carbonic anhydrase beta-CA1 [Coccomyxa sp. PA]
1523	LIB3602-064-Q1-K6-G5	6440928	BLASTX	790	2.00E-84	71	(AU066544) 60S ribosomal protein L2 [Chlamydomonas sp.]
1524	LIB3602-055-Q6-K1-E11	6440928	BLASTX	636	2.00E-66	80	(AU066544) 60S ribosomal protein L2 [Chlamydomonas sp.]
1525	LIB3602-116-Q1-K1-C10	6440928	BLASTX	487	1.00E-59	67	(AU066544) 60S ribosomal protein L2 [Chlamydomonas sp.]
1526	LIB3602-074-Q1-K1-B2	5734785	BLASTX	879	8.00E-95	81	(AC007980) phosphoprotein phosphatase [Arabidopsis thaliana]
1527	LIB3602-107-Q1-K1-B5	5734785	BLASTX	852	1.00E-91	84	(AC007980) phosphoprotein phosphatase [Arabidopsis thaliana]
1528	LIB3602-062-Q6-K1-H9	5734785	BLASTX	409	2.00E-75	73	(AC007980) phosphoprotein phosphatase [Arabidopsis thaliana]
1529	LIB3602-028-Q6-K1-C4	131199	BLASTX	201	2.00E-15	42	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT- HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 81470 pir S00453 photosystem I

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1530	LIB3602-014-Q6-K1-F2	131199	BLASTX	179	8.00E-13	40	protein psaH precursor - spinach >gi 21287 emb CAA34749.1 (X16858) psaH [Spinacia oleracea] PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 81470 pir S00453 photosystem I protein psaH precursor - spinach >gi 21287 emb CAA34749.1 (X16858) psaH [Spinacia oleracea]
1531	LIB3602-108-Q1-K1-G10	131199	BLASTX	149	1.00E-11	37	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 81470 pir S00453 photosystem I protein psaH precursor - spinach >gi 21287 emb CAA34749.1 (X16858) psaH [Spinacia oleracea]
1532	LIB3602-039-Q6-K1-G3	7630009	BLASTX	172	1.00E-12	63	(AL132960) 40S ribosomal protein S21 homolog [Arabidopsis thaliana]
1533	LIB3602-026-Q6-K1-C6	7630009	BLASTX	165	2.00E-11	60	(AL132960) 40S ribosomal protein S21 homolog [Arabidopsis thaliana]
1534	LIB3602-012-Q6-K1-A9	7630009	BLASTX	153	4.00E-10	60	(AL132960) 40S ribosomal protein S21 homolog [Arabidopsis thaliana]
1535	LIB3602-077-Q6-K6-D7	6647427	BLASTX	547	7.00E-56	73	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME) >gi 7437830 pir T03473 acetate--CoA ligase (EC 6.2.1.1) - Rhodobacter capsulatus >gi 3128274 gb AAC16126.1 (AF010496) acetyl-coenzyme a synthetase [Rhodobacter capsulatus]
1536	LIB3602-090-Q6-K6-E5	6647427	BLASTX	280	1.00E-24	69	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME) >gi 7437830 pir T03473 acetate--CoA ligase (EC 6.2.1.1) - Rhodobacter capsulatus >gi 3128274 gb AAC16126.1 (AF010496) acetyl-coenzyme a synthetase [Rhodobacter capsulatus]
1537	LIB3602-023-Q6-K1-E3	6647427	BLASTX	256	8.00E-22	69	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME) >gi 7437830 pir T03473 acetate--CoA ligase (EC 6.2.1.1) - Rhodobacter capsulatus >gi 3128274 gb AAC16126.1 (AF010496) acetyl-coenzyme a synthetase [Rhodobacter capsulatus]
1538	LIB3602-010-Q6-K1-G9	6325315	BLASTX	174	3.00E-12	36	putative mitochondrial carrier protein; Ymc1p >gi 1084942 pir S54080 carrier protein YMC1, mitochondrial - yeast (Saccharomyces cerevisiae) >gi 805039 emb CAA89176.1 (Z49219) Ymc1p [Saccharomyces cerevisiae] >gi 1314127 emb CAA95003.1 (Z71255) Ymc1p [S
1539	LIB3602-040-Q6-K1-F3	6325315	BLASTX	173	5.00E-12	38	putative mitochondrial carrier protein; Ymc1p >gi 1084942 pir S54080 carrier protein YMC1, mitochondrial - yeast (Saccharomyces cerevisiae) >gi 805039 emb CAA89176.1 (Z49219) Ymc1p [Saccharomyces cerevisiae] >gi 1314127 emb CAA95003.1 (Z71255) Ymc1p [S

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1540	LIB3602-070-Q1-K1-A6	6325315	BLASTX	170	1.00E-11	37	putative mitochondrial carrier protein; Ymc1p >gi 1084942 pir S54080 carrier protein YMC1, mitochondrial - yeast (<i>Saccharomyces cerevisiae</i>) >gi 805039 emb CAA89176.1 (Z49219) Ymc1p [<i>Saccharomyces cerevisiae</i>] >gi 1314127 emb CAA95003.1 (Z71255) Ymc1p [S
1541	LIB3602-094-Q6-K6-D7	6093778	BLASTX	733	1.00E-77	76	PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3) >gi 2511574 emb CAA73619.1 (Y13176) multicatalytic endopeptidase [<i>Arabidopsis thaliana</i>] >gi 3421075 gb AAC32056.1 (AF043520) 20S proteasome subunit PAB1 [Ar
1542	LIB3602-088-Q6-K6-G6	6093778	BLASTX	709	7.00E-75	76	PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3) >gi 2511574 emb CAA73619.1 (Y13176) multicatalytic endopeptidase [<i>Arabidopsis thaliana</i>] >gi 3421075 gb AAC32056.1 (AF043520) 20S proteasome subunit PAB1 [Ar
1543	LIB3602-118-Q1-K1-G6	6093778	BLASTX	545	2.00E-68	76	PROTEASOME COMPONENT C3 (MACROPAIN SUBUNIT C3) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C3) >gi 2511574 emb CAA73619.1 (Y13176) multicatalytic endopeptidase [<i>Arabidopsis thaliana</i>] >gi 3421075 gb AAC32056.1 (AF043520) 20S proteasome subunit PAB1 [Ar
1544	LIB3602-005-Q1-K1-A9	4557867	BLASTX	607	7.00E-63	59	sulfite oxidase >gi 1711606 sp P51687 SUOX_HUMAN SULFITE OXIDASE PRECURSOR >gi 1362942 pir S55874 sulfite oxidase (EC 1.8.3.1) precursor, mitochondrial - human >gi 508502 gb AAA74886.1 (L31573) sulfite oxidase [<i>Homo sapiens</i>] >gi 1098062 prf 2115221A su
1545	LIB3602-053-Q6-K1-A10	4557867	BLASTX	594	2.00E-61	60	sulfite oxidase >gi 1711606 sp P51687 SUOX_HUMAN SULFITE OXIDASE PRECURSOR >gi 1362942 pir S55874 sulfite oxidase (EC 1.8.3.1) precursor, mitochondrial - human >gi 508502 gb AAA74886.1 (L31573) sulfite oxidase [<i>Homo sapiens</i>] >gi 1098062 prf 2115221A su
1546	LIB3602-105-Q1-K1-C8	4557867	BLASTX	172	6.00E-12	45	sulfite oxidase >gi 1711606 sp P51687 SUOX_HUMAN SULFITE OXIDASE PRECURSOR >gi 1362942 pir S55874 sulfite oxidase (EC 1.8.3.1) precursor, mitochondrial - human >gi 508502 gb AAA74886.1 (L31573) sulfite oxidase [<i>Homo sapiens</i>] >gi 1098062 prf 2115221A su
1547	LIB3602-118-Q1-K1-A3	2688826	BLASTX	185	1.00E-13	52	(U95179) putative NifU protein [<i>Prunus armeniaca</i>]
1548	LIB3602-095-Q6-K6-F3	2688826	BLASTX	185	2.00E-13	52	(U95179) putative NifU protein [<i>Prunus armeniaca</i>]
1549	LIB3602-120-Q1-K1-D7	2688826	BLASTX	179	9.00E-13	50	(U95179) putative NifU protein [<i>Prunus armeniaca</i>]
1550	LIB3602-046-Q6-K1-A2	2583111	BLASTX	456	2.00E-45	58	(AC002387) putative dihydrodipicolinate synthase [<i>Arabidopsis thaliana</i>]
1551	LIB3602-012-Q6-K1-A8	2583111	BLASTX	430	4.00E-42	53	(AC002387) putative dihydrodipicolinate synthase [<i>Arabidopsis thaliana</i>]
1552	LIB3602-028-Q6-K1-C2	2583111	BLASTX	425	1.00E-41	70	(AC002387) putative dihydrodipicolinate synthase

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1553	LIB3602-056-Q6-K1-H9	1350996	BLASTX	515	3.00E-52	66	[Arabidopsis thaliana] 40S RIBOSOMAL PROTEIN S4 >gi 453574 dbj BAA05485.1 (D26473) Ribosomal Protein [Cricetulus griseus]
1554	LIB3602-116-Q1-K1-B12	1350996	BLASTX	338	5.00E-47	66	40S RIBOSOMAL PROTEIN S4 >gi 453574 dbj BAA05485.1 (D26473) Ribosomal Protein [Cricetulus griseus]
1555	LIB3602-056-Q6-K1-H10	1350996	BLASTX	236	2.00E-24	58	40S RIBOSOMAL PROTEIN S4 >gi 453574 dbj BAA05485.1 (D26473) Ribosomal Protein [Cricetulus griseus]
1556	LIB3602-032-Q6-K1-C6	7443230	BLASTX	245	9.00E-21	52	probable chlorophyll a/b-binding protein - rice >gi 3075488 gb AAC14566.1 (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
1557	LIB3602-019-Q6-K1-F11	7443230	BLASTX	239	7.00E-20	56	probable chlorophyll a/b-binding protein - rice >gi 3075488 gb AAC14566.1 (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
1558	LIB3602-059-Q6-K1-H2	7443230	BLASTX	227	1.00E-18	56	probable chlorophyll a/b-binding protein - rice >gi 3075488 gb AAC14566.1 (AF058796) chlorophyll a/b-binding protein [Oryza sativa]
1559	LIB3602-111-Q1-K1-G6	2500380	BLASTX	260	6.00E-35	84	60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir JC4923 ribosomal protein L36a.e, cytosolic - upland cotton >gi 1553129 gb AAB08726.1 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi 1553131 gb AAB08727.1 (U64678) ribosomal protein L44 isoform
1560	LIB3602-119-Q1-K1-D5	2500380	BLASTX	218	8.00E-31	76	60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir JC4923 ribosomal protein L36a.e, cytosolic - upland cotton >gi 1553129 gb AAB08726.1 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi 1553131 gb AAB08727.1 (U64678) ribosomal protein L44 isoform
1561	LIB3602-065-Q1-K6-A12	2500380	BLASTX	176	1.00E-22	63	60S RIBOSOMAL PROTEIN L44 >gi 2119128 pir JC4923 ribosomal protein L36a.e, cytosolic - upland cotton >gi 1553129 gb AAB08726.1 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi 1553131 gb AAB08727.1 (U64678) ribosomal protein L44 isoform
1562	LIB3602-089-Q6-K6-G11	7436330	BLASTX	444	8.00E-44	57	probable H ⁺ -transporting ATPase (EC 3.6.1.35) 18K chain - Arabidopsis thaliana >gi 4914450 emb CAB43690.1 (AL050398) H ⁺ -transporting ATPase-like protein [Arabidopsis thaliana] >gi 7270157 emb CAB79970.1 (AL161581) H ⁺ -transporting ATPase-like protein [Ar
1563	LIB3602-095-Q6-K6-G11	7436330	BLASTX	443	1.00E-43	56	probable H ⁺ -transporting ATPase (EC 3.6.1.35) 18K chain - Arabidopsis thaliana >gi 4914450 emb CAB43690.1 (AL050398) H ⁺ -transporting ATPase-like protein [Arabidopsis thaliana] >gi 7270157 emb CAB79970.1 (AL161581) H ⁺ -transporting ATPase-like protein [Ar
1564	LIB3602-112-Q1-K1-G11	7436330	BLASTX	443	1.00E-43	56	probable H ⁺ -transporting ATPase (EC 3.6.1.35) 18K chain - Arabidopsis thaliana >gi 4914450 emb CAB43690.1 (AL050398) H ⁺ -

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1565	LIB3602-089-Q6-K6-B9	6522577	BLASTX	310	3.00E-28	64	transporting ATPase-like protein [Arabidopsis thaliana] >gi 7270157 emb CAB79970.1 (AL161581) H+-transporting ATPase-like protein [Ar
1566	LIB3602-095-Q6-K6-B9	6522577	BLASTX	310	3.00E-28	64	(AL133292) putative helicase [Arabidopsis thaliana]
1567	LIB3602-116-Q1-K1-B9	6522577	BLASTX	195	7.00E-26	69	(AL133292) putative helicase [Arabidopsis thaliana]
1568	LIB3602-085-Q6-K1-C3	4775288	BLASTX	285	6.00E-36	61	(AJ238628) putative ferritin [Chlorella protothecoides]
1569	LIB3602-008-Q6-K1-B6	4775288	BLASTX	297	1.00E-26	61	(AJ238628) putative ferritin [Chlorella protothecoides]
1570	LIB3602-112-Q1-K1-C5	4775288	BLASTX	192	3.00E-14	55	(AJ238628) putative ferritin [Chlorella protothecoides]
1571	LIB3602-022-Q6-K1-G8	421766	BLASTX	213	7.00E-17	63	chlorophyll a/b-binding protein I-20 precursor - Chlamydomonas reinhardtii
1572	LIB3602-094-Q6-K6-F1	421766	BLASTX	208	3.00E-16	72	>gi 18125 emb CAA46235.1 (X65119) light harvesting complex protein I-20 [Chlamydomonas reinhardtii]
1573	LIB3602-104-Q1-K1-E4	421766	BLASTX	182	3.00E-13	68	chlorophyll a/b-binding protein I-20 precursor - Chlamydomonas reinhardtii
1574	LIB3602-120-Q1-K1-D12	1346750	BLASTX	665	6.00E-92	92	>gi 18125 emb CAA46235.1 (X65119) light harvesting complex protein I-20 [Chlamydomonas reinhardtii]
1575	LIB3602-107-Q1-K1-A2	1346750	BLASTX	720	3.00E-76	86	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1
1576	LIB3602-063-Q1-K6-C10	1346750	BLASTX	705	2.00E-74	88	>gi 2654372 emb CAA82263.1 (Z28627) protein phosphatase 1 [Acetabularia cliftonii]
1577	LIB3602-090-Q6-K6-H5	5080820	BLASTX	346	2.00E-32	35	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1
1578	LIB3602-114-Q1-K1-H5	5080820	BLASTX	346	3.00E-32	35	>gi 2654372 emb CAA82263.1 (Z28627) protein phosphatase 1 [Acetabularia cliftonii]
1579	LIB3602-040-Q6-K1-F5	5080820	BLASTX	209	2.00E-16	37	(AC007258) Putative ABC transporter [Arabidopsis thaliana]
1580	LIB3602-036-Q6-K1-A9	3334123	BLASTX	274	1.00E-37	39	(AC007258) Putative ABC transporter [Arabidopsis thaliana]
1581	LIB3602-030-Q6-K1-H11	3334123	BLASTX	304	2.00E-27	42	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
							>gi 1655480 dbj BAA13599.1 (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi 2924787 gb AAC04916.1 (AC002334) mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis t
							ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1582	LIB3602-120-Q1-K1-B7	3334123	BLASTX	178	1.00E-12	34	>gi 1655480 dbj BAA13599.1 (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi 2924787 gb AAC04916.1 (AC002334) mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis t ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi 1655480 dbj BAA13599.1 (D88374) gamma subunit of mitochondrial F1-ATPase [Arabidopsis thaliana] >gi 2924787 gb AAC04916.1 (AC002334) mitochondrial F1-ATPase, gamma subunit (ATP3_ARATH) [Arabidopsis t
1583	LIB3602-019-Q6-K1-F5	133883	BLASTX	445	3.00E-44	85	40S RIBOSOMAL PROTEIN S20 (S22) >gi 85846 pir A37974 ribosomal protein S20, cytosolic - African clawed frog >gi 214758 gb AAA49953.1 (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]
1584	LIB3602-004-Q1-K1-G10	133883	BLASTX	255	3.00E-32	70	40S RIBOSOMAL PROTEIN S20 (S22) >gi 85846 pir A37974 ribosomal protein S20, cytosolic - African clawed frog >gi 214758 gb AAA49953.1 (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]
1585	LIB3602-114-Q1-K1-D4	133883	BLASTX	169	3.00E-12	91	40S RIBOSOMAL PROTEIN S20 (S22) >gi 85846 pir A37974 ribosomal protein S20, cytosolic - African clawed frog >gi 214758 gb AAA49953.1 (M34706) ribosomal protein S22, 40S subunit [Xenopus laevis]
1586	LIB3602-003-Q1-K1-B11	7573429	BLASTX	244	2.00E-20	43	(AL163816) putative protein [Arabidopsis thaliana]
1587	LIB3602-056-Q6-K1-C9	7573429	BLASTX	169	1.00E-11	40	(AL163816) putative protein [Arabidopsis thaliana]
1588	LIB3602-003-Q1-K1-B5	7573429	BLASTX	152	1.00E-09	39	(AL163816) putative protein [Arabidopsis thaliana]
1589	LIB3602-026-Q6-K1-B10	5758304	BLASTX	479	6.00E-48	77	(AF161704) 40S ribosomal protein S17 [Lycopersicon esculentum]
1590	LIB3602-105-Q1-K1-H7	5758304	BLASTX	419	7.00E-41	73	(AF161704) 40S ribosomal protein S17 [Lycopersicon esculentum]
1591	LIB3602-065-Q1-K6-D4	5758304	BLASTX	325	6.00E-30	77	(AF161704) 40S ribosomal protein S17 [Lycopersicon esculentum]
1592	LIB3602-002-P1-K6-H6	7447940	BLASTX	289	1.00E-25	47	hypothetical protein slr1503 - Synechocystis sp. (strain PCC 6803) >gi 1653089 dbj BAA18005.1 (D90911) hypothetical protein [Synechocystis sp.]
1593	LIB3602-025-Q6-K1-F8	7447940	BLASTX	189	5.00E-14	44	hypothetical protein slr1503 - Synechocystis sp. (strain PCC 6803) >gi 1653089 dbj BAA18005.1 (D90911) hypothetical protein [Synechocystis sp.]
1594	LIB3602-047-Q6-K1-H5	7447940	BLASTX	167	8.00E-12	58	hypothetical protein slr1503 - Synechocystis sp. (strain PCC 6803) >gi 1653089 dbj BAA18005.1 (D90911) hypothetical protein [Synechocystis sp.]
1595	LIB3602-054-Q6-K1-D5	6015437	BLASTN	38	1.00E-12	100	Homo sapiens PEX1 mRNA, complete cds
1596	LIB3602-054-Q6-K1-E5	6015437	BLASTN	37	3.00E-11	100	Homo sapiens PEX1 mRNA, complete cds
1597	LIB3602-052-Q6-K1-B7	6015437	BLASTN	37	5.00E-11	100	Homo sapiens PEX1 mRNA, complete cds
1598	LIB3602-037-Q6-K1-D2	5360595	BLASTX	301	4.00E-27	42	(AB022330) nClpP5 [Arabidopsis thaliana]
1599	LIB3602-046-Q6-K1-H11	5360595	BLASTX	259	3.00E-22	61	(AB022330) nClpP5 [Arabidopsis thaliana]
1600	LIB3602-046-Q6-K1-H12	5360595	BLASTX	255	9.00E-22	60	(AB022330) nClpP5 [Arabidopsis thaliana]
1601	LIB3602-041-Q6-K1-G8	543696	BLASTX	656	1.00E-68	63	translation elongation factor EF-3 homolog - Chlorella virus CVK2 >gi 454301 dbj BAA03956.1 (D16505) translation elongation factor-3 [Chlorella virus]
1602	LIB3602-073-Q1-K1-F2	543696	BLASTX	488	8.00E-58	61	translation elongation factor EF-3 homolog -

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1603	LIB3602-095-Q6-K6-A1	543696	BLASTX	244	8.00E-21	55	Chlorella virus CVK2 >gi 454301 dbj BAA03956.1 (D16505) translation elongation factor-3 [Chlorella virus]
1604	LIB3602-015-Q6-K1-D10	7499991	BLASTX	277	3.00E-24	35	translation elongation factor EF-3 homolog - Chlorella virus CVK2 >gi 454301 dbj BAA03956.1 (D16505) translation elongation factor-3 [Chlorella virus]
1605	LIB3602-050-Q6-K1-H6	7499991	BLASTX	234	2.00E-19	40	hypothetical protein F27C1.7 - Caenorhabditis elegans >gi 1703605 gb AAB37654.1 (U80441) coded for by C. elegans cDNA yk63g10.5; coded for by C. elegans cDNA yk105c10.5; coded for by C. elegans cDNA yk167c12.5; coded for by C. elegans cDNA yk167c12.3; co
1606	LIB3602-074-Q1-K1-E12	7499991	BLASTX	214	8.00E-17	38	hypothetical protein F27C1.7 - Caenorhabditis elegans >gi 1703605 gb AAB37654.1 (U80441) coded for by C. elegans cDNA yk63g10.5; coded for by C. elegans cDNA yk105c10.5; coded for by C. elegans cDNA yk167c12.5; coded for by C. elegans cDNA yk167c12.3; co
1607	LIB3602-053-Q6-K1-D5	1245180	BLASTX	415	2.00E-40	47	(U49236) arginine deiminase [Giardia intestinalis]
1608	LIB3602-053-Q6-K1-D11	1245180	BLASTX	413	4.00E-40	47	(U49236) arginine deiminase [Giardia intestinalis]
1609	LIB3602-037-Q6-K1-H9	1245180	BLASTX	199	3.00E-15	45	(U49236) arginine deiminase [Giardia intestinalis]
1610	LIB3602-027-Q6-K1-F3	730449	BLASTX	390	2.00E-37	59	60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A) >gi 480647 pir S37132 ribosomal protein L13.A - rape >gi 398918 emb CAA80341.1 (Z22618) cold induced protein (BnC24A) [Brassica napus]
1611	LIB3602-009-Q6-K1-A2	730449	BLASTX	342	6.00E-32	55	60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A) >gi 480647 pir S37132 ribosomal protein L13.A - rape >gi 398918 emb CAA80341.1 (Z22618) cold induced protein (BnC24A) [Brassica napus]
1612	LIB3602-066-Q1-K6-D2	730449	BLASTX	296	1.00E-26	54	60S RIBOSOMAL PROTEIN L13-1 (COLD INDUCED PROTEIN C24A) >gi 480647 pir S37132 ribosomal protein L13.A - rape >gi 398918 emb CAA80341.1 (Z22618) cold induced protein (BnC24A) [Brassica napus]
1613	LIB3602-045-Q6-K1-B12	6552397	BLASTX	187	8.00E-14	73	(AB030493) thiamin biosynthetic enzyme [Glycine max]
1614	LIB3602-005-Q1-K1-G9	6552397	BLASTX	184	2.00E-13	68	(AB030493) thiamin biosynthetic enzyme [Glycine max]
1615	LIB3602-050-Q6-K1-G8	6552397	BLASTX	183	2.00E-13	76	(AB030493) thiamin biosynthetic enzyme [Glycine max]
1616	LIB3602-076-Q6-K6-A3	6714365	BLASTX	183	3.00E-13	47	(AC012562) unknown protein [Arabidopsis thaliana]
1617	LIB3602-069-Q1-K1-B1	6714365	BLASTX	181	6.00E-13	47	(AC012562) unknown protein [Arabidopsis thaliana]
1618	LIB3602-003-Q1-K1-A4	6714365	BLASTX	157	3.00E-10	50	(AC012562) unknown protein [Arabidopsis thaliana]
1619	LIB3602-089-Q6-K6-G9	3293539	BLASTX	469	9.00E-47	60	(AF072709) unknown [Streptomyces lividans]
1620	LIB3602-095-Q6-K6-G9	3293539	BLASTX	469	1.00E-46	60	(AF072709) unknown [Streptomyces lividans]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1621	LIB3602-112-Q1-K1-G9	3293539	BLASTX	469	1.00E-46	60	(AF072709) unknown [Streptomyces lividans]
1622	LIB3602-088-Q6-K6-H3	6456166	BLASTX	549	4.00E-56	74	(AC011622) GMP synthase [Arabidopsis thaliana]
1623	LIB3602-104-Q1-K1-E6	6456166	BLASTX	548	5.00E-56	73	(AC011622) GMP synthase [Arabidopsis thaliana]
1624	LIB3602-061-Q6-K1-H12	6456166	BLASTX	455	3.00E-45	75	(AC011622) GMP synthase [Arabidopsis thaliana]
1625	LIB3602-111-Q1-K1-C10	7447845	BLASTX	553	9.00E-57	76	hypothetical protein T16L1.170 - Arabidopsis thaliana >gi 3549670 emb CAA20581.1 (AL031394) putative protein [Arabidopsis thaliana] >gi 7270317 emb CAB80085.1 (AL161584) putative protein [Arabidopsis thaliana]
1626	LIB3602-006-Q1-K1-B10	7447845	BLASTX	362	3.00E-34	73	hypothetical protein T16L1.170 - Arabidopsis thaliana >gi 3549670 emb CAA20581.1 (AL031394) putative protein [Arabidopsis thaliana] >gi 7270317 emb CAB80085.1 (AL161584) putative protein [Arabidopsis thaliana]
1627	LIB3602-043-Q6-K1-E11	7447845	BLASTX	299	4.00E-27	57	hypothetical protein T16L1.170 - Arabidopsis thaliana >gi 3549670 emb CAA20581.1 (AL031394) putative protein [Arabidopsis thaliana] >gi 7270317 emb CAB80085.1 (AL161584) putative protein [Arabidopsis thaliana]
1628	LIB3602-066-Q1-K6-C3	7019650	BLASTX	278	2.00E-24	63	(AL132954) ribosomal protein L35-like [Arabidopsis thaliana]
1629	LIB3602-117-Q1-K1-C8	7019650	BLASTX	157	9.00E-13	63	(AL132954) ribosomal protein L35-like [Arabidopsis thaliana]
1630	LIB3602-044-Q6-K1-D10	7019650	BLASTX	145	1.00E-10	51	(AL132954) ribosomal protein L35-like [Arabidopsis thaliana]
1631	LIB3602-044-Q6-K1-H9	2501354	BLASTX	509	1.00E-51	65	TRANSKETOLASE 7 (TK) >gi 1084441 pir S54301 transketolase (EC 2.2.1.1) 7 - Craterostigma plantagineum >gi 664903 emb CAA86609.1 (Z46648) transketolase [Craterostigma plantagineum]
1632	LIB3602-055-Q6-K1-H2	2501354	BLASTX	479	5.00E-48	61	TRANSKETOLASE 7 (TK) >gi 1084441 pir S54301 transketolase (EC 2.2.1.1) 7 - Craterostigma plantagineum >gi 664903 emb CAA86609.1 (Z46648) transketolase [Craterostigma plantagineum]
1633	LIB3602-044-Q6-K1-H10	2501354	BLASTX	219	1.00E-17	45	TRANSKETOLASE 7 (TK) >gi 1084441 pir S54301 transketolase (EC 2.2.1.1) 7 - Craterostigma plantagineum >gi 664903 emb CAA86609.1 (Z46648) transketolase [Craterostigma plantagineum]
1634	LIB3602-030-Q6-K1-G6	7023084	BLASTX	183	2.00E-13	35	(AK001677) unnamed protein product [Homo sapiens]
1635	LIB3602-093-Q6-K6-C6	7023084	BLASTX	161	1.00E-10	37	(AK001677) unnamed protein product [Homo sapiens]
1636	LIB3602-113-Q1-K1-G1	7023084	BLASTX	161	1.00E-10	37	(AK001677) unnamed protein product [Homo sapiens]
1637	LIB3602-109-Q1-K1-E10	7485750	BLASTX	413	3.00E-40	52	hypothetical protein F19B15.90 - Arabidopsis thaliana >gi 4972052 emb CAB43920.1 (AL078470) putative protein [Arabidopsis thaliana] >gi 7269804 emb CAB79664.1 (AL161574) putative protein [Arabidopsis thaliana]
1638	LIB3602-078-Q6-K6-B7	7485750	BLASTX	269	3.00E-23	60	hypothetical protein F19B15.90 - Arabidopsis thaliana >gi 4972052 emb CAB43920.1 (AL078470) putative protein [Arabidopsis thaliana] >gi 7269804 emb CAB79664.1 (AL161574) putative protein [Arabidopsis thaliana]
1639	LIB3602-068-Q1-K1-E7	7485750	BLASTX	263	1.00E-22	60	hypothetical protein F19B15.90 - Arabidopsis

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							thaliana >gi 4972052 emb CAB43920.1 (AL078470) putative protein [Arabidopsis thaliana] >gi 7269804 emb CAB79664.1 (AL161574) putative protein [Arabidopsis thaliana]
1640	LIB3602-094-Q6-K6-E12	1902882	BLASTX	202	1.00E-15	47	(AB001833) ribosomal protein YL16 homolog [Schizosaccharomyces pombe]
1641	LIB3602-091-Q6-K6-E12	1902882	BLASTX	193	2.00E-14	50	(AB001833) ribosomal protein YL16 homolog [Schizosaccharomyces pombe]
1642	LIB3602-040-Q6-K1-A2	1902882	BLASTX	148	1.00E-09	60	(AB001833) ribosomal protein YL16 homolog [Schizosaccharomyces pombe]
1643	LIB3602-115-Q1-K1-C1	7441176	BLASTX	330	1.00E-30	60	ribosomal protein L35, cytosolic - Arabidopsis thaliana >gi 3355468 gb AAC27830.1 (AC004218) 60S ribosomal protein L35 [Arabidopsis thaliana]
1644	LIB3602-013-Q6-K1-D1	7441176	BLASTX	238	3.00E-20	59	ribosomal protein L35, cytosolic - Arabidopsis thaliana >gi 3355468 gb AAC27830.1 (AC004218) 60S ribosomal protein L35 [Arabidopsis thaliana]
1645	LIB3602-070-Q1-K1-E5	7441176	BLASTX	235	8.00E-20	59	ribosomal protein L35, cytosolic - Arabidopsis thaliana >gi 3355468 gb AAC27830.1 (AC004218) 60S ribosomal protein L35 [Arabidopsis thaliana]
1646	LIB3602-108-Q1-K1-G1	3885884	BLASTX	340	6.00E-32	65	(AF093630) 60S ribosomal protein L21 [Oryza sativa]
1647	LIB3602-106-Q1-K1-B3	3885884	BLASTX	223	6.00E-18	41	(AF093630) 60S ribosomal protein L21 [Oryza sativa]
1648	LIB3602-051-Q6-K1-D12	3885884	BLASTX	150	5.00E-10	47	(AF093630) 60S ribosomal protein L21 [Oryza sativa]
1649	LIB3602-020-Q6-K1-B9	2851583	BLASTX	242	3.00E-20	58	ALPHA-AMYLASE TYPE B ISOZYME PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (AMY2-2) (HIGH PI ALPHA-AMYLASE) >gi 1070490 pir ALBHB alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley >gi 166995 gb AAA98790.1 (K02637) Hordeum vulgare alpha-amylase type
1650	LIB3602-074-Q1-K1-D2	2851583	BLASTX	212	1.00E-16	54	ALPHA-AMYLASE TYPE B ISOZYME PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (AMY2-2) (HIGH PI ALPHA-AMYLASE) >gi 1070490 pir ALBHB alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley >gi 166995 gb AAA98790.1 (K02637) Hordeum vulgare alpha-amylase type
1651	LIB3602-032-Q6-K1-A10	2851583	BLASTX	189	4.00E-14	56	ALPHA-AMYLASE TYPE B ISOZYME PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) (AMY2-2) (HIGH PI ALPHA-AMYLASE) >gi 1070490 pir ALBHB alpha-amylase (EC 3.2.1.1) B precursor 6-4 - barley >gi 166995 gb AAA98790.1 (K02637) Hordeum vulgare alpha-amylase type
1652	LIB3602-087-Q6-K1-A4	132167	BLASTX	795	5.00E-85	87	RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 320539 pir A45507 ribulose-bisphosphate carboxylase activase (EC 6.3.4.-) precursor - Chlamydomonas reinhardtii >gi 167434 gb AAA33091.1 (M62962) ribulose
1653	LIB3602-084-Q6-K1-A4	132167	BLASTX	774	2.00E-82	81	RIBULOSE BISPHTHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 320539 pir A45507 ribulose-bisphosphate carboxylase activase (EC 6.3.4.-)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1654	LIB3602-050-Q6-K1-C1	132167	BLASTX	760	5.00E-81	96	precursor - Chlamydomonas reinhardtii >gi 167434 gb AAA33091.1 (M62962) ribulose RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi 320539 pir A45507 ribulose-bisphosphate carboxylase activase (EC 6.3.4.-)
1655	LIB3602-095-Q6-K6-A5	117971	BLASTX	429	5.00E-42	79	precursor - Chlamydomonas reinhardtii >gi 167434 gb AAA33091.1 (M62962) ribulose CYTOCHROME C >gi 322374 pir S29514 cytochrome c - Chlamydomonas reinhardtii >gi 167413 gb AAA33084.1 (M35173) apocytochrome c (cyc) [Chlamydomonas reinhardtii] >gi 2660500 emb CAB16954.1 (Z99829) cytochrome c [Chlamydomonas reinhardtii] >gi 226382 prf
1656	LIB3602-117-Q1-K1-D12	117971	BLASTX	396	2.00E-38	82	CYTOCHROME C >gi 322374 pir S29514 cytochrome c - Chlamydomonas reinhardtii >gi 167413 gb AAA33084.1 (M35173) apocytochrome c (cyc) [Chlamydomonas reinhardtii] >gi 2660500 emb CAB16954.1 (Z99829) cytochrome c [Chlamydomonas reinhardtii] >gi 226382 prf
1657	LIB3602-013-Q6-K1-C1	117971	BLASTX	246	1.00E-20	85	CYTOCHROME C >gi 322374 pir S29514 cytochrome c - Chlamydomonas reinhardtii >gi 167413 gb AAA33084.1 (M35173) apocytochrome c (cyc) [Chlamydomonas reinhardtii] >gi 2660500 emb CAB16954.1 (Z99829) cytochrome c [Chlamydomonas reinhardtii] >gi 226382 prf
1658	LIB3602-014-Q6-K1-H9	3913425	BLASTX	387	3.00E-37	69	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 gb AAB63825.1 (AC002337) putative pre-mRNA splicing factor RNA helicase [Arabidopsis thaliana]
1659	LIB3602-035-Q1-K1-G10	3913425	BLASTX	371	2.00E-35	67	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 gb AAB63825.1 (AC002337) putative pre-mRNA splicing factor RNA helicase [Arabidopsis thaliana]
1660	LIB3602-034-Q6-K1-G10	3913425	BLASTX	312	1.00E-28	63	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi 2275203 gb AAB63825.1 (AC002337) putative pre-mRNA splicing factor RNA helicase [Arabidopsis thaliana]
1661	LIB3602-118-Q1-K1-G11	167427	BLASTN	46	1.00E-16	90	C.reinhardtii oxygen-evolving enhancer protein 2 (OEE2) mRNA, complete cds
1662	LIB3602-094-Q6-K6-F12	167427	BLASTN	46	2.00E-16	90	C.reinhardtii oxygen-evolving enhancer protein 2 (OEE2) mRNA, complete cds
1663	LIB3602-114-Q1-K1-D11	167427	BLASTN	46	3.00E-16	90	C.reinhardtii oxygen-evolving enhancer protein 2 (OEE2) mRNA, complete cds
1664	LIB3602-109-Q1-K1-G1	7487122	BLASTX	265	7.00E-25	43	hypothetical protein T17F15.230 - Arabidopsis thaliana >gi 4678338 emb CAB41149.1 (AL049658) putative protein [Arabidopsis thaliana]
1665	LIB3602-058-Q6-K1-B11	7487122	BLASTX	197	5.00E-15	41	hypothetical protein T17F15.230 - Arabidopsis thaliana >gi 4678338 emb CAB41149.1 (AL049658) putative protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1666	LIB3602-012-Q6-K1-B10	7487122	BLASTX	198	6.00E-15	28	hypothetical protein T17F15.230 - Arabidopsis thaliana >gi 4678338 emb CAB41149.1 (AL049658) putative protein [Arabidopsis thaliana]
1667	LIB3602-076-Q6-K6-C2	6752882	BLASTX	317	6.00E-29	53	(AF220200) nascent polypeptide associated complex alpha chain [Pinus taeda]
1668	LIB3602-105-Q1-K1-H4	6752882	BLASTX	309	5.00E-28	52	(AF220200) nascent polypeptide associated complex alpha chain [Pinus taeda]
1669	LIB3602-050-Q6-K1-A5	6752882	BLASTX	280	1.00E-24	78	(AF220200) nascent polypeptide associated complex alpha chain [Pinus taeda]
1670	LIB3602-023-Q6-K1-E2	4107276	BLASTX	440	5.00E-47	66	(X98506) acetyl-CoA synthetase [Solanum tuberosum]
1671	LIB3602-089-Q6-K6-F4	4107276	BLASTX	179	9.00E-13	69	(X98506) acetyl-CoA synthetase [Solanum tuberosum]
1672	LIB3602-056-Q6-K1-F3	4107276	BLASTX	178	9.00E-13	76	(X98506) acetyl-CoA synthetase [Solanum tuberosum]
1673	LIB3602-060-Q6-K1-C7	421985	BLASTX	311	2.00E-28	79	ribosomal protein L17.1, cytosolic - barley
1674	LIB3602-015-Q6-K1-C3	421985	BLASTX	275	3.00E-24	79	ribosomal protein L17.1, cytosolic - barley
1675	LIB3602-036-Q6-K1-B8	421985	BLASTX	245	1.00E-20	76	ribosomal protein L17.1, cytosolic - barley
1676	LIB3602-003-Q1-K1-C8	5019305	BLASTX	252	2.00E-21	33	(AJ011563) carnitine/acyl carnitine carrier [Emericella nidulans]
1677	LIB3602-039-Q6-K1-C7	5019305	BLASTX	251	3.00E-21	35	(AJ011563) carnitine/acyl carnitine carrier [Emericella nidulans]
1678	LIB3602-003-Q1-K1-C9	5019305	BLASTX	178	9.00E-13	33	(AJ011563) carnitine/acyl carnitine carrier [Emericella nidulans]
1679	LIB3602-034-Q6-K1-C6	5174741	BLASTX	394	5.00E-38	52	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) >gi 136682 sp P15374 UBL3_HUMAN UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3) (UBIQUITIN THIOLESTERASE L3) >gi 108014 pir A40085 ubiquitin thiolesterase (EC 3.1.2.15) L3 - huma
1680	LIB3602-104-Q1-K1-D11	5174741	BLASTX	393	8.00E-38	52	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) >gi 136682 sp P15374 UBL3_HUMAN UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3) (UBIQUITIN THIOLESTERASE L3) >gi 108014 pir A40085 ubiquitin thiolesterase (EC 3.1.2.15) L3 - huma
1681	LIB3602-035-Q1-K1-C6	5174741	BLASTX	356	1.00E-33	54	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) >gi 136682 sp P15374 UBL3_HUMAN UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3) (UBIQUITIN THIOLESTERASE L3) >gi 108014 pir A40085 ubiquitin thiolesterase (EC 3.1.2.15) L3 - huma
1682	LIB3602-050-Q6-K1-B11	7446976	BLASTX	589	6.00E-61	73	1-deoxy-D-xylulose-5-phosphate synthase precursor - Chlamydomonas reinhardtii >gi 4185881 emb CAA07554.1 (AJ007559) 1-deoxy-D-xylulose-5-phosphate synthase [Chlamydomonas reinhardtii]
1683	LIB3602-109-Q1-K1-E5	7446976	BLASTX	429	1.00E-58	69	1-deoxy-D-xylulose-5-phosphate synthase precursor - Chlamydomonas reinhardtii >gi 4185881 emb CAA07554.1 (AJ007559) 1-deoxy-D-xylulose-5-phosphate synthase

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1684	LIB3602-020-Q6-K1-H8	7446976	BLASTX	521	7.00E-53	65	[Chlamydomonas reinhardtii] 1-deoxy-D-xylulose-5-phosphate synthase precursor - Chlamydomonas reinhardtii >gi 4185881 emb CAA07554.1 (AJ007559) 1-deoxy-D-xylulose-5-phosphate synthase [Chlamydomonas reinhardtii]
1685	LIB3602-064-Q1-K6-A2	238318	BLASTX	578	2.00E-59	58	(S62652) branched-chain alpha-keto acid dehydrogenase E1 alpha subunit [human, Peptide, 443 aa] [Homo sapiens]
1686	LIB3602-076-Q6-K6-H5	238318	BLASTX	544	2.00E-55	55	(S62652) branched-chain alpha-keto acid dehydrogenase E1 alpha subunit [human, Peptide, 443 aa] [Homo sapiens]
1687	LIB3602-022-Q6-K1-A10	238318	BLASTX	177	1.00E-12	40	(S62652) branched-chain alpha-keto acid dehydrogenase E1 alpha subunit [human, Peptide, 443 aa] [Homo sapiens]
1688	LIB3602-012-Q6-K1-C3	7485188	BLASTX	484	2.00E-48	58	hypothetical protein - Arabidopsis thaliana >gi 2245118 emb CAB10540.1 (Z97343) hypothetical protein [Arabidopsis thaliana] >gi 7268512 emb CAB78763.1 (AL161546) hypothetical protein [Arabidopsis thaliana]
1689	LIB3602-032-Q6-K1-H9	7485188	BLASTX	389	2.00E-37	57	hypothetical protein - Arabidopsis thaliana >gi 2245118 emb CAB10540.1 (Z97343) hypothetical protein [Arabidopsis thaliana] >gi 7268512 emb CAB78763.1 (AL161546) hypothetical protein [Arabidopsis thaliana]
1690	LIB3602-027-Q6-K1-A10	7485188	BLASTX	384	8.00E-37	60	hypothetical protein - Arabidopsis thaliana >gi 2245118 emb CAB10540.1 (Z97343) hypothetical protein [Arabidopsis thaliana] >gi 7268512 emb CAB78763.1 (AL161546) hypothetical protein [Arabidopsis thaliana]
1691	LIB3602-054-Q6-K1-A2	3915826	BLASTX	207	3.00E-16	51	60S RIBOSOMAL PROTEIN L5
1692	LIB3602-053-Q6-K1-H11	3915826	BLASTX	159	1.00E-10	55	60S RIBOSOMAL PROTEIN L5
1693	LIB3602-052-Q6-K1-C9	3915826	BLASTX	145	6.00E-09	53	60S RIBOSOMAL PROTEIN L5
1694	LIB3602-088-Q6-K6-C5	7435750	BLASTX	362	3.00E-34	51	cell division control protein 48, AAA family (cdc48-2) homolog - Archaeoglobus fulgidus >gi 2648442 gb AAB89157.1 (AE000959) cell division control protein 48, AAA family (cdc48-2) [Archaeoglobus fulgidus]
1695	LIB3602-118-Q1-K1-C5	7435750	BLASTX	348	1.00E-32	52	cell division control protein 48, AAA family (cdc48-2) homolog - Archaeoglobus fulgidus >gi 2648442 gb AAB89157.1 (AE000959) cell division control protein 48, AAA family (cdc48-2) [Archaeoglobus fulgidus]
1696	LIB3602-090-Q6-K6-F2	7435750	BLASTX	331	1.00E-30	48	cell division control protein 48, AAA family (cdc48-2) homolog - Archaeoglobus fulgidus >gi 2648442 gb AAB89157.1 (AE000959) cell division control protein 48, AAA family (cdc48-2) [Archaeoglobus fulgidus]
1697	LIB3602-104-Q1-K1-H9	7384996	BLASTX	185	2.00E-13	49	(AF153422) lacZ [Cloning vector pTG8]
1698	LIB3602-100-Q1-K1-C11	7384996	BLASTX	161	6.00E-11	43	(AF153422) lacZ [Cloning vector pTG8]
1699	LIB3602-055-Q6-K1-H7	7384996	BLASTX	157	2.00E-10	37	(AF153422) lacZ [Cloning vector pTG8]
1700	LIB3602-093-Q6-K6-B7	416222	BLASTX	585	2.00E-60	98	(D16504) alpha-tubulin [Chlorella vulgaris]
1701	LIB3602-104-Q1-K1-B7	416222	BLASTX	554	9.00E-57	99	(D16504) alpha-tubulin [Chlorella vulgaris]
1702	LIB3602-117-Q1-K1-B7	416222	BLASTX	263	1.00E-43	100	(D16504) alpha-tubulin [Chlorella vulgaris]
1703	LIB3602-002-P1-K6-E5	6056208	BLASTX	440	2.00E-43	50	(AC009400) putative ATPase [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1704	LIB3602-065-Q1-K6-D5	6056208	BLASTX	191	2.00E-14	50	(AC009400) putative ATPase [Arabidopsis thaliana]
1705	LIB3602-111-Q1-K1-A1	6056208	BLASTX	187	5.00E-14	50	(AC009400) putative ATPase [Arabidopsis thaliana]
1706	LIB3602-029-Q6-K1-C10	1351122	BLASTX	502	1.00E-50	68	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR (STRESS-INDUCIBLE PROTEIN STI35) >gi 280494 pir B37767 stress-inducible protein sti35 - fungus (Fusarium oxysporum) >gi 168164 gb AAA33341.1 (M33643) STI35 protein [Fusarium oxysporum] >gi 6045153 dbj BAA85305.1 (
1707	LIB3602-088-Q6-K6-G1	1351122	BLASTX	477	1.00E-47	67	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR (STRESS-INDUCIBLE PROTEIN STI35) >gi 280494 pir B37767 stress-inducible protein sti35 - fungus (Fusarium oxysporum) >gi 168164 gb AAA33341.1 (M33643) STI35 protein [Fusarium oxysporum] >gi 6045153 dbj BAA85305.1 (
1708	LIB3602-103-Q1-K1-G10	1351122	BLASTX	391	1.00E-37	66	THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR (STRESS-INDUCIBLE PROTEIN STI35) >gi 280494 pir B37767 stress-inducible protein sti35 - fungus (Fusarium oxysporum) >gi 168164 gb AAA33341.1 (M33643) STI35 protein [Fusarium oxysporum] >gi 6045153 dbj BAA85305.1 (
1709	LIB3602-062-Q6-K1-A9	3806118	BLASTX	182	1.00E-13	79	(AF097201) 40S ribosomal protein S8 [Schizophyllum commune]
1710	LIB3602-062-Q6-K1-A10	3806118	BLASTX	181	1.00E-13	75	(AF097201) 40S ribosomal protein S8 [Schizophyllum commune]
1711	LIB3602-007-Q1-K1-E11	3806118	BLASTX	165	9.00E-12	84	(AF097201) 40S ribosomal protein S8 [Schizophyllum commune]
1712	LIB3602-113-Q1-K1-G6	132099	BLASTX	189	3.00E-14	92	RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN PW9 PRECURSOR (RUBISCO SMALL SUBUNIT PW9) >gi 68091 pir RKWTS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pW9) - wheat >gi 170771 gb AAA34302.1 (M37477) ribulose-1,5-bisphos
1713	LIB3602-092-Q6-K6-G6	132099	BLASTX	185	8.00E-14	97	RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN PW9 PRECURSOR (RUBISCO SMALL SUBUNIT PW9) >gi 68091 pir RKWTS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pW9) - wheat >gi 170771 gb AAA34302.1 (M37477) ribulose-1,5-bisphos
1714	LIB3602-120-Q1-K1-G6	132099	BLASTX	172	2.00E-12	100	RIBULOSE BIPHOSPHATE CARBOXYLASE SMALL CHAIN PW9 PRECURSOR (RUBISCO SMALL SUBUNIT PW9) >gi 68091 pir RKWTS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pW9) - wheat >gi 170771 gb AAA34302.1 (M37477) ribulose-1,5-bisphos
1715	LIB3602-109-Q1-K1-F3	6554488	BLASTX	343	4.00E-32	62	(AC012394) putative small nuclear ribonucleoprotein Sm D3 [Arabidopsis thaliana] >gi 6573711 gb AAF17631.1 AC009978_7 (AC009978) T23E18.23 [Arabidopsis thaliana]
1716	LIB3602-074-Q1-K1-G10	6554488	BLASTX	327	4.00E-30	61	(AC012394) putative small nuclear ribonucleoprotein Sm D3 [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1717	LIB3602-107-Q1-K1-A9	6554488	BLASTX	319	3.00E-29	62	>gi 6573711 gb AAF17631.1 AC009978_7 (AC009978) T23E18.23 [Arabidopsis thaliana] (AC012394) putative small nuclear ribonucleoprotein Sm D3 [Arabidopsis thaliana]
1718	LIB3602-074-Q1-K1-H11	417103	BLASTX	627	3.00E-65	99	>gi 6573711 gb AAF17631.1 AC009978_7 (AC009978) T23E18.23 [Arabidopsis thaliana] HISTONE H3.2, MINOR >gi 282871 pir S24346 histone H3.3-like protein - Arabidopsis thaliana >gi 16324 emb CAA42957.1 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958.1 (X60429) histone H3.3 like protein [Arabidopsis thal
1719	LIB3602-087-Q6-K1-E12	417103	BLASTX	425	1.00E-58	98	HISTONE H3.2, MINOR >gi 282871 pir S24346 histone H3.3-like protein - Arabidopsis thaliana >gi 16324 emb CAA42957.1 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958.1 (X60429) histone H3.3 like protein [Arabidopsis thal
1720	LIB3602-007-Q1-K1-C5	417103	BLASTX	539	6.00E-55	94	HISTONE H3.2, MINOR >gi 282871 pir S24346 histone H3.3-like protein - Arabidopsis thaliana >gi 16324 emb CAA42957.1 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958.1 (X60429) histone H3.3 like protein [Arabidopsis thal
1721	LIB3602-073-Q1-K1-G3	4512679	BLASTX	595	2.00E-61	80	(AC006931) 60S ribosomal protein L11B [Arabidopsis thaliana]
1722	LIB3602-017-Q6-K1-E1	4512679	BLASTX	484	1.00E-48	84	(AC006931) 60S ribosomal protein L11B [Arabidopsis thaliana]
1723	LIB3602-009-Q6-K1-H9	4512679	BLASTX	309	3.00E-28	82	(AC006931) 60S ribosomal protein L11B [Arabidopsis thaliana]
1724	LIB3602-040-Q6-K1-H4	7488407	BLASTX	308	4.00E-28	55	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 14K chain - Arabidopsis thaliana >gi 4049349 emb CAA22574.1 (AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana] >gi 7270151 emb CAB79964.1 (AL161581) ubiquinol-cytochrome c redu
1725	LIB3602-108-Q1-K1-H11	7488407	BLASTX	277	2.00E-24	53	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 14K chain - Arabidopsis thaliana >gi 4049349 emb CAA22574.1 (AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana] >gi 7270151 emb CAB79964.1 (AL161581) ubiquinol-cytochrome c redu
1726	LIB3602-046-Q6-K1-D4	7488407	BLASTX	236	1.00E-19	63	ubiquinol--cytochrome-c reductase (EC 1.10.2.2) 14K chain - Arabidopsis thaliana >gi 4049349 emb CAA22574.1 (AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana] >gi 7270151 emb CAB79964.1 (AL161581) ubiquinol-cytochrome c redu
1727	LIB3602-040-Q6-K1-F1	131183	BLASTX	315	8.00E-29	63	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) (P21 PROTEIN) >gi 81244 pir S04133 photosystem I chain III precursor - Chlamydomonas reinhardtii >gi 18184 emb CAA31849.1 (X13495) P21 precursor prote

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1728	LIB3602-045-Q6-K1-B8	131183	BLASTX	290	7.00E-26	61	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) (P21 PROTEIN) >gi 81244 pir S04133 photosystem I chain III precursor - Chlamydomonas reinhardtii >gi 18184 emb CAA31849.1 (X13495) P21 precursor prote
1729	LIB3602-114-Q1-K1-C1	131183	BLASTX	288	1.00E-25	62	PHOTOSYSTEM I REACTION CENTRE SUBUNIT III PRECURSOR (LIGHT-HARVESTING COMPLEX I 17 KD PROTEIN) (PSI-F) (P21 PROTEIN) >gi 81244 pir S04133 photosystem I chain III precursor - Chlamydomonas reinhardtii >gi 18184 emb CAA31849.1 (X13495) P21 precursor prote
1730	LIB3602-019-Q6-K1-H12	3914658	BLASTX	331	1.00E-30	47	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi 1694974 emb CAA70851.1 (Y09635) plastid ribosomal protein [Arabidopsis thaliana]
1731	LIB3602-025-Q6-K1-F11	3914658	BLASTX	331	1.00E-30	47	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi 1694974 emb CAA70851.1 (Y09635) plastid ribosomal protein [Arabidopsis thaliana]
1732	LIB3602-083-Q6-K6-B7	3914658	BLASTX	331	2.00E-30	47	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR >gi 1694974 emb CAA70851.1 (Y09635) plastid ribosomal protein [Arabidopsis thaliana]
1733	LIB3602-073-Q1-K1-E6	7428008	BLASTX	565	5.00E-58	54	calcium-dependent protein kinase (EC 2.7.1.-), calmodulin-independent - maize (fragment) >gi 639722 gb AAA61682.1 (L27484) calcium-dependent protein kinase [Zea mays]
1734	LIB3602-093-Q6-K6-F10	7428008	BLASTX	288	2.00E-25	45	calcium-dependent protein kinase (EC 2.7.1.-), calmodulin-independent - maize (fragment) >gi 639722 gb AAA61682.1 (L27484) calcium-dependent protein kinase [Zea mays]
1735	LIB3602-119-Q1-K1-F10	7428008	BLASTX	273	5.00E-24	45	calcium-dependent protein kinase (EC 2.7.1.-), calmodulin-independent - maize (fragment) >gi 639722 gb AAA61682.1 (L27484) calcium-dependent protein kinase [Zea mays]
1736	LIB3602-040-Q6-K1-A5	5902365	BLASTX	662	1.00E-69	86	(AC009322) Putative splicing factor Prp8 [Arabidopsis thaliana]
1737	LIB3602-054-Q6-K1-F12	5902365	BLASTX	177	1.00E-12	50	(AC009322) Putative splicing factor Prp8 [Arabidopsis thaliana]
1738	LIB3602-056-Q6-K1-D12	2492861	BLASTX	561	1.00E-57	77	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi 629466 pir S43787 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Chlamydomonas reinhardtii >gi 424151 gb AAA18861.1 (U03632) gluta
1739	LIB3602-044-Q6-K1-G6	2492861	BLASTX	555	6.00E-57	76	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi 629466 pir S43787 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - Chlamydomonas reinhardtii >gi 424151 gb AAA18861.1 (U03632) gluta

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1740	LIB3602-035-Q1-K1-B11	6647650	BLASTX	504	8.00E-54	62	NADH-UBIQUINONE OXIDOREDUCTASE 24 KD SUBUNIT PRECURSOR >gi 7427765 pir T01091 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 24K chain homolog - Arabidopsis thaliana >gi 3892051 gb AAC78260.1 AAC78260 (AC002330) predicted NADH dehydrogenase 24 kD subunit [
1741	LIB3602-034-Q6-K1-B11	6647650	BLASTX	490	3.00E-49	61	NADH-UBIQUINONE OXIDOREDUCTASE 24 KD SUBUNIT PRECURSOR >gi 7427765 pir T01091 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 24K chain homolog - Arabidopsis thaliana >gi 3892051 gb AAC78260.1 AAC78260 (AC002330) predicted NADH dehydrogenase 24 kD subunit [
1742	LIB3602-106-Q1-K1-B10	7438140	BLASTX	521	8.00E-53	67	acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxylase chain precursor - soybean >gi 3219361 gb AAC23573.1 (AF068249) biotin carboxylase precursor [Glycine max]
1743	LIB3602-100-Q1-K1-B10	7438140	BLASTX	485	1.00E-48	65	acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxylase chain precursor - soybean >gi 3219361 gb AAC23573.1 (AF068249) biotin carboxylase precursor [Glycine max]
1744	LIB3602-085-Q6-K1-F9	115575	BLASTX	447	4.00E-44	51	PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) >gi 68032 pir QYIX1 phosphoenolpyruvate carboxylase (EC 4.1.1.31) 1 - common ice plant >gi 19536 emb CAA31956.1 (X13660) phosphoenolpyruvate carboxylase (AA 1 - 966) [Mesembryanthemum crystallinum] >gi 22559 e
1745	LIB3602-022-Q6-K1-A2	115575	BLASTX	338	1.00E-31	50	PHOSPHOENOLPYRUVATE CARBOXYLASE 1 (PEPCASE) >gi 68032 pir QYIX1 phosphoenolpyruvate carboxylase (EC 4.1.1.31) 1 - common ice plant >gi 19536 emb CAA31956.1 (X13660) phosphoenolpyruvate carboxylase (AA 1 - 966) [Mesembryanthemum crystallinum] >gi 22559 e
1746	LIB3602-078-Q6-K6-C7	7437844	BLASTX	382	2.00E-36	46	probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) isoform 1 - rape >gi 1617268 emb CAA96523.1 (Z72153) acyl CoA synthetase [Brassica napus]
1747	LIB3602-038-Q6-K1-B7	7437844	BLASTX	301	4.00E-27	47	probable long-chain-fatty-acid--CoA ligase (EC 6.2.1.3) isoform 1 - rape >gi 1617268 emb CAA96523.1 (Z72153) acyl CoA synthetase [Brassica napus]
1748	LIB3602-040-Q6-K1-G4	166985	BLASTX	532	3.00E-54	60	(J04202) alpha-amylase [Hordeum vulgare]
1749	LIB3602-056-Q6-K1-E11	166985	BLASTX	500	1.00E-50	64	(J04202) alpha-amylase [Hordeum vulgare]
1750	LIB3602-085-Q6-K1-D6	5708095	BLASTX	524	3.00E-53	59	(AJ245502) ATP synthase gamma chain, chloroplast precursor [Arabidopsis thaliana]
1751	LIB3602-063-Q1-K6-E7	5708095	BLASTX	493	1.00E-49	55	(AJ245502) ATP synthase gamma chain, chloroplast precursor [Arabidopsis thaliana]
1752	LIB3602-014-Q6-K1-H2	7481092	BLASTX	273	7.00E-24	52	probable oxidoreductase - Streptomyces coelicolor >gi 2815335 emb CAA16459.1 (AL021529) SC10A5.27c, possible oxidoreductase, len: 326 aa; so me similarity to many members of the SHORT-CHAIN DEHYDROGEN ASEs/REDUCTASES

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1753	LIB3602-058-Q6-K1-G9	7481092	BLASTX	191	2.00E-14	40	FAMILY (SDR) eg. YGFF_ECOLI P52037 hy probable oxidoreductase - Streptomyces coelicolor >gi 2815335 emb CAA16459.1 (AL021529) SC10A5.27c, possible oxidoreductase, len: 326 aa; so me similarity to many members of the SHORT-CHAIN DEHYDROGEN ASES/REDUCTASES FAMILY (SDR) eg. YGFF_ECOLI P52037 hy
1754	LIB3602-073-Q1-K1-A3	5902400	BLASTX	419	7.00E-41	51	(AC008148) Unknown protein [Arabidopsis thaliana]
1755	LIB3602-010-Q6-K1-G11	5902400	BLASTX	410	7.00E-40	50	(AC008148) Unknown protein [Arabidopsis thaliana]
1756	LIB3602-019-Q6-K1-G6	6403490	BLASTX	375	9.00E-36	51	(AC010871) putative SCO1 protein [Arabidopsis thaliana]
1757	LIB3602-057-Q6-K1-E4	6403490	BLASTX	321	2.00E-29	60	(AC010871) putative SCO1 protein [Arabidopsis thaliana]
1758	LIB3602-041-Q6-K1-D10	322391	BLASTX	346	2.00E-32	51	chlorophyll a/b-binding protein Lhcb5 - Scotch pine >gi 22750 emb CAA78900.1 (Z16408) Lhcb5 protein [Pinus sylvestris] >gi 1093837 prf 2104448A Lhcb5 gene [Pinus sylvestris]
1759	LIB3602-072-Q1-K1-D5	322391	BLASTX	346	3.00E-32	51	chlorophyll a/b-binding protein Lhcb5 - Scotch pine >gi 22750 emb CAA78900.1 (Z16408) Lhcb5 protein [Pinus sylvestris] >gi 1093837 prf 2104448A Lhcb5 gene [Pinus sylvestris]
1760	LIB3602-047-Q6-K1-F10	2494745	BLASTX	385	5.00E-37	81	GLUTAMINE SYNTHETASE, CHLOROPLAST PRECURSOR (GLUTAMATE--AMMONIA LIGASE) (GS2) >gi 7437923 pir T08090 probable glutamate--ammonia ligase (EC 6.3.1.2), chloroplast - Chlamydomonas reinhardtii >gi 1353878 gb AAB01818.1 (U46208) glutamine synthetase [Chlamy
1761	LIB3602-090-Q6-K6-D5	2494745	BLASTX	256	2.00E-22	78	GLUTAMINE SYNTHETASE, CHLOROPLAST PRECURSOR (GLUTAMATE--AMMONIA LIGASE) (GS2) >gi 7437923 pir T08090 probable glutamate--ammonia ligase (EC 6.3.1.2), chloroplast - Chlamydomonas reinhardtii >gi 1353878 gb AAB01818.1 (U46208) glutamine synthetase [Chlamy
1762	LIB3602-062-Q6-K1-B4	6671953	BLASTX	401	8.00E-39	62	(AC016795) putative pre-rRNA processing protein, 5' partial [Arabidopsis thaliana]
1763	LIB3602-062-Q6-K1-B5	6671953	BLASTX	245	1.00E-20	53	(AC016795) putative pre-rRNA processing protein, 5' partial [Arabidopsis thaliana]
1764	LIB3602-074-Q1-K1-E4	1085669	BLASTX	197	6.00E-15	38	methylcrotonoyl-CoA carboxylase (EC 6.4.1.4) biotin-binding chain - tomato (fragment) >gi 497181 gb AAA19157.1 (U07745) biotin-containing subunit of methylcrotonoyl-CoA carboxylase [Lycopersicon esculentum]
1765	LIB3602-087-Q6-K1-H6	1085669	BLASTX	197	7.00E-15	38	methylcrotonoyl-CoA carboxylase (EC 6.4.1.4) biotin-binding chain - tomato (fragment) >gi 497181 gb AAA19157.1 (U07745) biotin-containing subunit of methylcrotonoyl-CoA carboxylase [Lycopersicon esculentum]
1766	LIB3602-077-Q6-K6-H8	1730560	BLASTX	226	3.00E-18	63	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi 7433824 pir T12091 starch phosphorylase (EC 2.4.1.1) H, cytosolic isoform - fava bean

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1767	LIB3602-088-Q6-K6-D10	1730560	BLASTX	226	3.00E-18	63	>gi 510932 emb CAA84494.1 (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba] ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi 7433824 pir T12091 starch phosphorylase (EC 2.4.1.1) H, cytosolic isoform - fava bean >gi 510932 emb CAA84494.1 (Z35117) alpha 1,4-glucan phosphorylase type H [Vicia faba]
1768	LIB3602-016-Q6-K1-D10	7487536	BLASTX	332	8.00E-31	48	hypothetical protein T29H11.60 - Arabidopsis thaliana >gi 4678346 emb CAB41156.1 (AL049659) putative protein [Arabidopsis thaliana]
1769	LIB3602-017-Q6-K1-B4	7487536	BLASTX	182	3.00E-13	72	hypothetical protein T29H11.60 - Arabidopsis thaliana >gi 4678346 emb CAB41156.1 (AL049659) putative protein [Arabidopsis thaliana]
1770	LIB3602-025-Q6-K1-A12	6468487	BLASTX	352	4.00E-33	68	(AJ251083) putative cytosolic malate dehydrogenase [Beta vulgaris]
1771	LIB3602-037-Q6-K1-C12	6468487	BLASTX	235	2.00E-19	71	(AJ251083) putative cytosolic malate dehydrogenase [Beta vulgaris]
1772	LIB3602-050-Q6-K1-B10	167408	BLASTN	38	1.00E-11	91	C.reinhardtii encoding chlorophyll a/b-binding protein (cabII-1) gene, complete cds
1773	LIB3602-019-Q6-K1-A6	167408	BLASTN	33	9.00E-09	89	C.reinhardtii encoding chlorophyll a/b-binding protein (cabII-1) gene, complete cds
1774	LIB3602-011-Q6-K1-D11	4115942	BLASTX	212	1.00E-16	50	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=238.4, E= 1e-67, N=1) and EF hand domains (Pfam: PF00036, score=109.0, E=8.9e-29, N=5) [Arabidopsis thaliana] >gi 7267229 emb CAB80836.1 (AL161501) putative calcium
1775	LIB3602-053-Q6-K1-B11	4115942	BLASTX	153	1.00E-09	49	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=238.4, E= 1e-67, N=1) and EF hand domains (Pfam: PF00036, score=109.0, E=8.9e-29, N=5) [Arabidopsis thaliana] >gi 7267229 emb CAB80836.1 (AL161501) putative calcium
1776	LIB3602-064-Q1-K6-F10	7485715	BLASTX	288	1.00E-25	59	hypothetical protein F18E5.180 - Arabidopsis thaliana >gi 3080400 emb CAA18720.1 (AL022603) putative protein [Arabidopsis thaliana] >gi 4455264 emb CAB36800.1 (AL035527) putative protein [Arabidopsis thaliana] >gi 7268953 emb CAB81263.1 (AL161555) puta
1777	LIB3602-059-Q6-K1-B7	7485715	BLASTX	173	2.00E-12	50	hypothetical protein F18E5.180 - Arabidopsis thaliana >gi 3080400 emb CAA18720.1 (AL022603) putative protein [Arabidopsis thaliana] >gi 4455264 emb CAB36800.1 (AL035527) putative protein [Arabidopsis thaliana] >gi 7268953 emb CAB81263.1 (AL161555) puta
1778	LIB3602-053-Q6-K1-G7	4514360	BLASTX	234	2.00E-19	63	(AB013377) BsaA [Bacillus halodurans]
1779	LIB3602-055-Q6-K1-D11	4514360	BLASTX	216	3.00E-17	68	(AB013377) BsaA [Bacillus halodurans]
1780	LIB3602-109-Q1-K1-H8	2232057	BLASTX	230	9.00E-19	59	(AF000177) CaSm [Homo sapiens] >gi 5262854 emb CAB45865.1 (AJ238094) Lsm1 protein [Homo sapiens]
1781	LIB3602-083-Q6-K6-H8	2232057	BLASTX	230	1.00E-18	59	(AF000177) CaSm [Homo sapiens] >gi 5262854 emb CAB45865.1 (AJ238094) Lsm1 protein [Homo sapiens]
1782	LIB3602-025-Q6-K1-C4	2462781	BLASTX	617	4.00E-64	67	(U73175) carbamoyl phosphate synthetase small

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1783	LIB3602-002-P1-K6-H9	2462781	BLASTX	254	1.00E-21	62	subunit [Arabidopsis thaliana] (U73175) carbamoyl phosphate synthetase small
1784	LIB3602-093-Q6-K6-C8	7381458	BLASTX	472	4.00E-47	56	subunit [Arabidopsis thaliana] (AF210322) UMP synthase [Oryza sativa]
1785	LIB3602-104-Q1-K1-C8	7381458	BLASTX	437	5.00E-43	57	(AF210322) UMP synthase [Oryza sativa]
1786	LIB3602-104-Q1-K1-G9	1419687	BLASTX	425	1.00E-41	50	(X98825) 40-kDa V-ATPase subunit [Manduca sexta]
1787	LIB3602-093-Q6-K6-G9	1419687	BLASTX	424	2.00E-41	50	(X98825) 40-kDa V-ATPase subunit [Manduca sexta]
1788	LIB3602-095-Q6-K6-H1	2117676	BLASTX	692	7.00E-73	65	superoxide dismutase (EC 1.15.1.1) (Fe) precursor - Chlamydomonas reinhardtii >gi 726293 gb AAB04944.1 (U22416) superoxide dismutase precursor [Chlamydomonas reinhardtii]
1789	LIB3602-077-Q6-K6-F8	2117676	BLASTX	421	1.00E-42	66	superoxide dismutase (EC 1.15.1.1) (Fe) precursor - Chlamydomonas reinhardtii >gi 726293 gb AAB04944.1 (U22416) superoxide dismutase precursor [Chlamydomonas reinhardtii]
1790	LIB3602-059-Q6-K1-B1	6466939	BLASTX	177	1.00E-12	49	(AC009176) unknown protein, 5' partial [Arabidopsis thaliana]
1791	LIB3602-059-Q6-K1-B2	6466939	BLASTX	175	3.00E-12	47	(AC009176) unknown protein, 5' partial [Arabidopsis thaliana]
1792	LIB3602-067-Q1-K1-A8	6911856	BLASTX	248	2.00E-30	88	(AL138649) putative protein [Arabidopsis thaliana]
1793	LIB3602-084-Q6-K1-G11	6911856	BLASTX	193	8.00E-26	81	(AL138649) putative protein [Arabidopsis thaliana]
1794	LIB3602-072-Q1-K1-B8	130264	BLASTX	231	2.00E-19	77	PLASTOCYANIN PRECURSOR (PC6-2) >gi 99419 pir A36569 plastocyanin precursor - Chlamydomonas reinhardtii >gi 167401 gb AAA33078.1 (J05524) apoplastocyanin (PC6-2) precursor [Chlamydomonas reinhardtii] >gi 167430 gb AAA33089.1 (L07282) plastocyanin [Chlam
1795	LIB3602-040-Q6-K1-F8	130264	BLASTX	227	6.00E-19	78	PLASTOCYANIN PRECURSOR (PC6-2) >gi 99419 pir A36569 plastocyanin precursor - Chlamydomonas reinhardtii >gi 167401 gb AAA33078.1 (J05524) apoplastocyanin (PC6-2) precursor [Chlamydomonas reinhardtii] >gi 167430 gb AAA33089.1 (L07282) plastocyanin [Chlam
1796	LIB3602-060-Q6-K1-H1	4530100	BLASTX	345	3.00E-32	43	(AF063418) elongation factor 1-alpha [Enchytraeus sp. 'Enc']
1797	LIB3602-063-Q1-K6-F10	4530100	BLASTX	272	8.00E-24	42	(AF063418) elongation factor 1-alpha [Enchytraeus sp. 'Enc']
1798	LIB3602-059-Q6-K1-G2	6907102	BLASTX	218	2.00E-17	66	(AP001129) ESTs AU032852(S15362),AU070591(S5037) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid T10C6. (Z93388) [Oryza sativa]
1799	LIB3602-059-Q6-K1-G3	6907102	BLASTX	189	5.00E-14	45	(AP001129) ESTs AU032852(S15362),AU070591(S5037) correspond to a region of the predicted gene.; Similar to Caenorhabditis elegans cosmid T10C6. (Z93388) [Oryza sativa]
1800	LIB3602-070-Q1-K1-D8	7340289	BLASTX	251	4.00E-21	44	(AF245222) OP1 [Cucumis sativus]
1801	LIB3602-076-Q6-K6-B9	7340289	BLASTX	251	4.00E-21	44	(AF245222) OP1 [Cucumis sativus]
1802	LIB3602-070-Q1-K1-A5	4972728	BLASTX	529	9.00E-54	57	(AF132171) unknown [Drosophila melanogaster]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1803	LIB3602-001-P1-K6-F12	4972728	BLASTX	382	1.00E-36	55	>gi 7300952 gb AAF56091.1 (AE003741) BcDNA:LD21504 gene product [Drosophila melanogaster]
1804	LIB3602-045-Q6-K1-D11	914284	BLASTX	232	4.00E-19	84	(AF132171) unknown [Drosophila melanogaster] >gi 7300952 gb AAF56091.1 (AE003741) BcDNA:LD21504 gene product [Drosophila melanogaster]
1805	LIB3602-058-Q6-K1-C10	914284	BLASTX	232	4.00E-19	84	light-harvesting complex b type 3, Lhcb3 [Ginkgo biloba, 3-4 week old seedlings, Peptide Partial, 132 aa]
1806	LIB3602-076-Q6-K6-C11	4731372	BLASTX	191	4.00E-14	46	light-harvesting complex b type 3, Lhcb3 [Ginkgo biloba, 3-4 week old seedlings, Peptide Partial, 132 aa]
1807	LIB3602-112-Q1-K1-H2	4731372	BLASTX	175	3.00E-12	44	(AF133838) papain-like cysteine protease [Sandersonia aurantiaca]
1808	LIB3602-050-Q6-K1-A12	6599226	BLASTX	346	2.00E-32	46	(AF133838) papain-like cysteine protease [Sandersonia aurantiaca]
1809	LIB3602-050-Q6-K1-A11	6599226	BLASTX	305	1.00E-27	42	(AL133613) hypothetical protein [Homo sapiens]
1810	LIB3602-115-Q1-K1-D7	7433571	BLASTX	636	2.00E-66	67	(AL133613) hypothetical protein [Homo sapiens]
1811	LIB3602-115-Q1-K1-A7	7433571	BLASTX	550	2.00E-56	65	probable phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) - Arabidopsis thaliana >gi 3033398 gb AAC12842.1 (AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]
1812	LIB3602-005-Q1-K1-C11	3915430	BLASTX	280	1.00E-24	59	probable phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) - Arabidopsis thaliana >gi 3033398 gb AAC12842.1 (AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]
1813	LIB3602-078-Q6-K6-C3	3915430	BLASTX	267	3.00E-23	60	HYPOTHETICAL 11.3 KD PROTEIN IN RIBE-PYKF INTERGENIC REGION PRECURSOR >gi 7459798 pir C64924 hypothetical protein b1667 - Escherichia coli >gi 1549278 gb AAB47943.1 (U68703) hypothetical protein [Escherichia coli]
1814	LIB3602-109-Q1-K1-B2	7484357	BLASTX	515	9.00E-63	83	>gi 1787956 gb AAC74737.1 (AE000262) o HYPOTHETICAL 11.3 KD PROTEIN IN RIBE-PYKF INTERGENIC REGION PRECURSOR >gi 7459798 pir C64924 hypothetical protein b1667 - Escherichia coli >gi 1549278 gb AAB47943.1 (U68703) hypothetical protein [Escherichia coli]
1815	LIB3602-040-Q6-K1-F9	7484357	BLASTX	233	3.00E-19	74	>gi 1787956 gb AAC74737.1 (AE000262) o carbonate dehydratase (EC 4.2.1.1) 2 beta, mitochondrial - Chlamydomonas reinhardtii >gi 1737488 gb AAC49888.1 (U80805) beta-carbonic anhydrase [Chlamydomonas reinhardtii]
1816	LIB3602-004-Q1-K1-D9	7298333	BLASTX	185	2.00E-13	32	carbonate dehydratase (EC 4.2.1.1) 2 beta, mitochondrial - Chlamydomonas reinhardtii >gi 1737488 gb AAC49888.1 (U80805) beta-carbonic anhydrase [Chlamydomonas reinhardtii]
1817	LIB3602-085-Q6-K1-E3	7298333	BLASTX	171	9.00E-12	29	(AE003652) CG17905 gene product [Drosophila melanogaster]
							(AE003652) CG17905 gene product [Drosophila melanogaster]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1818	LIB3602-029-Q6-K1-A4	7435330	BLASTX	412	4.00E-40	48	alpha-amylase (EC 3.2.1.1) - Arabidopsis thaliana >gi 4455243 emb CAB36742.1 (AL035523) alpha-amylase-like protein [Arabidopsis thaliana] >gi 7269350 emb CAB79409.1 (AL161562) alpha-amylase-like protein [Arabidopsis thaliana]
1819	LIB3602-051-Q6-K1-F9	7435330	BLASTX	401	7.00E-39	50	alpha-amylase (EC 3.2.1.1) - Arabidopsis thaliana >gi 4455243 emb CAB36742.1 (AL035523) alpha-amylase-like protein [Arabidopsis thaliana] >gi 7269350 emb CAB79409.1 (AL161562) alpha-amylase-like protein [Arabidopsis thaliana]
1820	LIB3602-108-Q1-K1-F10	7443228	BLASTX	188	6.00E-18	63	chlorophyll a/b-binding protein F24G24.140 - Arabidopsis thaliana >gi 4538963 emb CAB39787.1 (AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] >gi 7
1821	LIB3602-052-Q6-K1-E6	7443228	BLASTX	163	4.00E-11	59	chlorophyll a/b-binding protein F24G24.140 - Arabidopsis thaliana >gi 4538963 emb CAB39787.1 (AL049488) chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129_1 (AF134129) Lhcb5 protein [Arabidopsis thaliana] >gi 7
1822	LIB3602-014-Q6-K1-H11	7442279	BLASTX	295	2.00E-26	60	probable acyl carrier protein T8F5.6 - Arabidopsis thaliana >gi 3335337 gb AAC27139.1 (AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb L23574 from A. thaliana. ESTs gb
1823	LIB3602-044-Q6-K1-E5	7442279	BLASTX	283	5.00E-25	67	probable acyl carrier protein T8F5.6 - Arabidopsis thaliana >gi 3335337 gb AAC27139.1 (AC004512) Similar to acyl carrier protein, mitochondrial precursor (ACP) NADH-ubiquinone oxidoreductase 9.6 KD subunit (MYACP-1), gb L23574 from A. thaliana. ESTs gb
1824	LIB3602-113-Q1-K1-E4	4558549	BLASTX	710	5.00E-75	71	(AC007138) putative SecA-type chloroplast protein transport factor [Arabidopsis thaliana] >gi 7268223 emb CAB77750.1 (AL161492) putative SecA-type chloroplast protein transport factor [Arabidopsis thaliana]
1825	LIB3602-114-Q1-K1-F7	4558549	BLASTX	700	8.00E-74	71	(AC007138) putative SecA-type chloroplast protein transport factor [Arabidopsis thaliana] >gi 7268223 emb CAB77750.1 (AL161492) putative SecA-type chloroplast protein transport factor [Arabidopsis thaliana]
1826	LIB3602-103-Q1-K1-F7	3107919	BLASTX	792	1.00E-84	95	(AB013098) actin [Nannochloris bacillaris]
1827	LIB3602-109-Q1-K1-G10	3107919	BLASTX	672	1.00E-70	90	(AB013098) actin [Nannochloris bacillaris]
1828	LIB3602-084-Q6-K1-H9	6984130	BLASTX	688	4.00E-73	82	(AF227620) 60S ribosomal protein L10 [Euphorbia esula]
1829	LIB3602-007-Q1-K1-G2	6984130	BLASTX	264	4.00E-46	94	(AF227620) 60S ribosomal protein L10 [Euphorbia esula]
1830	LIB3602-072-Q1-K1-A8	3122234	BLASTX	477	1.00E-47	63	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) (P38) >gi 7450843 pir T06992 translation initiation factor

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1831	LIB3602-109-Q1-K1-D12	3122234	BLASTX	210	8.00E-31	59	eIF-2 beta chain - wheat >gi 2306768 gb AAB65774.1 (U87163) eIF-2 beta subunit [Triticum aestivum] EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) (P38) >gi 7450843 pir T06992 translation initiation factor eIF-2 beta chain - wheat >gi 2306768 gb AAB65774.1 (U87163) eIF-2 beta subunit [Triticum aestivum]
1832	LIB3602-034-Q6-K1-C7	6523090	BLASTX	296	1.00E-26	71	(AL133315) transcription factor Hap5a [Arabidopsis thaliana]
1833	LIB3602-035-Q1-K1-C7	6523090	BLASTX	291	5.00E-26	71	(AL133315) transcription factor Hap5a [Arabidopsis thaliana]
1834	LIB3602-027-Q6-K1-E5	3122707	BLASTX	292	4.00E-26	58	50S RIBOSOMAL PROTEIN L24 >gi 2446901 dbj BAA22460.1 (AB000111) 50S ribosomal protein L24 [Synechococcus sp.]
1835	LIB3602-109-Q1-K1-B7	3122707	BLASTX	246	9.00E-21	58	50S RIBOSOMAL PROTEIN L24 >gi 2446901 dbj BAA22460.1 (AB000111) 50S ribosomal protein L24 [Synechococcus sp.]
1836	LIB3602-062-Q6-K1-B2	1173071	BLASTX	181	3.00E-13	41	60S ACIDIC RIBOSOMAL PROTEIN P2 (MINOR ALLERGEN ALT A 6) (ALT A VI) >gi 1085614 pir S43109 acidic ribosomal protein P2 - Alternaria alternata >gi 467617 emb CAA55066.1 (X78222) minor allergen, ribosomal protein [Alternaria alternata]
1837	LIB3602-057-Q6-K1-D10	1173071	BLASTX	157	2.00E-10	40	60S ACIDIC RIBOSOMAL PROTEIN P2 (MINOR ALLERGEN ALT A 6) (ALT A VI) >gi 1085614 pir S43109 acidic ribosomal protein P2 - Alternaria alternata >gi 467617 emb CAA55066.1 (X78222) minor allergen, ribosomal protein [Alternaria alternata]
1838	LIB3602-010-Q6-K1-G10	1173070	BLASTX	201	2.00E-15	52	50S RIBOSOMAL PROTEIN L9 >gi 485508 pir S33614 ribosomal protein L9 - Synechocystis sp. (strain PCC 6803) >gi 217101 dbj BAA38819.1 (D10716) 50S ribosomal protein L9 [Synechocystis sp.] >gi 1653258 dbj BAA18173.1 (D90912) 50S ribosomal protein L9 [Syne
1839	LIB3602-011-Q6-K1-B7	1173070	BLASTX	176	2.00E-12	38	50S RIBOSOMAL PROTEIN L9 >gi 485508 pir S33614 ribosomal protein L9 - Synechocystis sp. (strain PCC 6803) >gi 217101 dbj BAA38819.1 (D10716) 50S ribosomal protein L9 [Synechocystis sp.] >gi 1653258 dbj BAA18173.1 (D90912) 50S ribosomal protein L9 [Syne
1840	LIB3602-056-Q6-K1-C1	2765356	BLASTX	556	4.00E-57	80	(Y13865) chlorophyll a/b-binding protein [Beta vulgaris]
1841	LIB3602-013-Q6-K1-E5	2765356	BLASTX	535	1.00E-54	80	(Y13865) chlorophyll a/b-binding protein [Beta vulgaris]
1842	LIB3602-076-Q6-K6-D3	3024019	BLASTX	586	2.00E-60	74	INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi 2225879 dbj BAA20876.1 (AB004823) eukaryotic initiation factor 5A2 [Solanum tuberosum] >gi 2225887 dbj BAA20880.1 (AB004827) eukaryotic initiation factor 5A1 [Solanum tuberosum]
1843	LIB3602-061-Q6-K1-F3	3024019	BLASTX	353	3.00E-33	66	INITIATION FACTOR 5A (EIF-5A) (EIF-4D) >gi 2225879 dbj BAA20876.1 (AB004823) eukaryotic initiation factor 5A2 [Solanum

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1844	LIB3602-007-Q1-K1-E10	543867	BLASTX	431	3.00E-42	52	tuberosum] >gi 2225887 dbj BAA20880.1 (AB004827) eukaryotic initiation factor 5A1 [Solanum tuberosum] ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi 1076684 pir A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi 303626 dbj BAA03526.1 (D14699) F1-ATPase gamma subunit [Ipomoea batatas]
1845	LIB3602-072-Q1-K1-D4	543867	BLASTX	385	6.00E-37	60	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi 1076684 pir A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, mitochondrial - sweet potato >gi 303626 dbj BAA03526.1 (D14699) F1-ATPase gamma subunit [Ipomoea batatas]
1846	LIB3602-032-Q6-K1-F1	3293547	BLASTX	298	8.00E-27	46	(AF072709) putative oxidoreductase [Streptomyces lividans]
1847	LIB3602-023-Q6-K1-F1	3293547	BLASTX	215	5.00E-17	33	(AF072709) putative oxidoreductase [Streptomyces lividans]
1848	LIB3602-032-Q6-K1-B4	7024455	BLASTX	588	7.00E-61	77	(AB034696) vacuolar-pyrophosphatase like protein [Arabidopsis thaliana]
1849	LIB3602-050-Q6-K1-C4	7024455	BLASTX	238	7.00E-20	77	(AB034696) vacuolar-pyrophosphatase like protein [Arabidopsis thaliana]
1850	LIB3602-118-Q1-K1-F12	5052206	BLASTX	216	4.00E-17	38	(AF100198) putative NAD(P)H steroid dehydrogenase [Mus musculus] >gi 7619723 emb CAA15948.2 (AL021127) NAD(P)H steroid dehydrogenase [Mus musculus]
1851	LIB3602-105-Q1-K1-C4	5052206	BLASTX	211	2.00E-16	38	(AF100198) putative NAD(P)H steroid dehydrogenase [Mus musculus] >gi 7619723 emb CAA15948.2 (AL021127) NAD(P)H steroid dehydrogenase [Mus musculus]
1852	LIB3602-070-Q1-K1-F7	7297921	BLASTX	674	9.00E-71	63	(AE003635) CG5353 gene product [alt 1] [Drosophila melanogaster] >gi 7297922 gb AAF53167.1 (AE003635) CG5353 gene product [alt 2] [Drosophila melanogaster]
1853	LIB3602-012-Q6-K1-B7	7297921	BLASTX	493	1.00E-49	56	(AE003635) CG5353 gene product [alt 1] [Drosophila melanogaster] >gi 7297922 gb AAF53167.1 (AE003635) CG5353 gene product [alt 2] [Drosophila melanogaster]
1854	LIB3602-058-Q6-K1-H3	2129459	BLASTX	612	1.00E-63	76	chaperonin 60 alpha chain precursor, chloroplast - Chlamydomonas reinhardtii
1855	LIB3602-017-Q6-K1-G3	2129459	BLASTX	214	7.00E-17	62	chaperonin 60 alpha chain precursor, chloroplast - Chlamydomonas reinhardtii
1856	LIB3602-076-Q6-K6-G5	3776005	BLASTX	386	5.00E-37	83	(AJ010466) RNA helicase [Arabidopsis thaliana]
1857	LIB3602-076-Q6-K6-H1	3776005	BLASTX	149	2.00E-09	83	(AJ010466) RNA helicase [Arabidopsis thaliana]
1858	LIB3602-066-Q1-K6-G2	2911276	BLASTX	174	4.00E-12	70	(U63631) LMW heat shock protein [Fragaria x ananassa]
1859	LIB3602-106-Q1-K1-B1	2911276	BLASTX	174	4.00E-12	70	(U63631) LMW heat shock protein [Fragaria x ananassa]
1860	LIB3602-100-Q1-K1-G3	7484780	BLASTX	447	4.00E-44	46	26S proteasome regulatory particle chain RPN7 homolog F6I7.30 - Arabidopsis thaliana >gi 4678261 emb CAB41122.1 (AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana] >gi 7269333 emb CAB79392.1 (AL161562) putative proteasome regulatory

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1861	LIB3602-106-Q1-K1-G3	7484780	BLASTX	419	7.00E-41	45	26S proteasome regulatory particle chain RPN7 homolog F6I7.30 - Arabidopsis thaliana >gi 4678261 emb CAB41122.1 (AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana] >gi 7269333 emb CAB79392.1 (AL161562) putative proteasome regulatory
1862	LIB3602-100-Q1-K1-H7	2494116	BLASTX	352	4.00E-33	52	(AC002376) Similar to Synechocystis hypothetical protein (gb D90915). [Arabidopsis thaliana]
1863	LIB3602-106-Q1-K1-H7	2494116	BLASTX	297	1.00E-27	51	(AC002376) Similar to Synechocystis hypothetical protein (gb D90915). [Arabidopsis thaliana]
1864	LIB3602-026-Q6-K1-H2	7262687	BLASTX	147	5.00E-09	45	(AC012188) Contains similarity to an unknown protein from Arabidopsis thaliana gb AC004136.2. ESTs gb Z47683, gb Z47682, gb AA597850, gb Z29736, gb Z29735, gb AA042623 come from this gene
1865	LIB3602-036-Q6-K1-C9	7262687	BLASTX	147	6.00E-09	45	(AC012188) Contains similarity to an unknown protein from Arabidopsis thaliana gb AC004136.2. ESTs gb Z47683, gb Z47682, gb AA597850, gb Z29736, gb Z29735, gb AA042623 come from this gene
1866	LIB3602-084-Q6-K1-E12	4049408	BLASTX	278	2.00E-24	52	(Y10224) L-ascorbate oxidase [Cucumis melo]
1867	LIB3602-095-Q6-K6-B2	4049408	BLASTX	166	3.00E-11	54	(Y10224) L-ascorbate oxidase [Cucumis melo]
1868	LIB3602-034-Q6-K1-E8	5921663	BLASTX	745	4.00E-79	76	(AF162279) 10-formyltetrahydrofolate synthetase [Arabidopsis thaliana]
1869	LIB3602-035-Q1-K1-E8	5921663	BLASTX	665	1.00E-71	76	(AF162279) 10-formyltetrahydrofolate synthetase [Arabidopsis thaliana]
1870	LIB3602-003-Q1-K1-G9	6010630	BLASTX	184	2.00E-13	41	(AF179401) TspO [Sinorhizobium meliloti]
1871	LIB3602-050-Q6-K1-E7	6010630	BLASTX	167	2.00E-11	48	(AF179401) TspO [Sinorhizobium meliloti]
1872	LIB3602-114-Q1-K1-F8	280386	BLASTX	318	5.00E-43	90	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi 166930 gb AAA32904.1 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi 166932 gb AAA32905.1 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi 488626
1873	LIB3602-116-Q1-K1-C3	280386	BLASTX	170	3.00E-15	60	ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana >gi 166930 gb AAA32904.1 (J05507) ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi 166932 gb AAA32905.1 (J05508) ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi 488626
1874	LIB3602-013-Q6-K1-G6	82080	BLASTX	445	4.00E-44	66	chlorophyll a/b-binding protein type III precursor - tomato >gi 226872 prf 1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]
1875	LIB3602-058-Q6-K1-F8	82080	BLASTX	352	4.00E-33	69	chlorophyll a/b-binding protein type III precursor - tomato >gi 226872 prf 1609235A chlorophyll a/b binding protein [Lycopersicon esculentum]
1876	LIB3602-067-Q1-K1-F5	7437318	BLASTX	649	8.00E-68	73	peptidylprolyl isomerase (EC 5.2.1.8) 1 - Chlamydomonas reinhardtii >gi 2959712 gb AAC05639.1 (AF052206) cyclophilin 1 [Chlamydomonas reinhardtii]
1877	LIB3602-085-Q6-K1-C10	7437318	BLASTX	642	5.00E-67	72	peptidylprolyl isomerase (EC 5.2.1.8) 1 - Chlamydomonas reinhardtii >gi 2959712 gb AAC05639.1 (AF052206) cyclophilin 1 [Chlamydomonas reinhardtii]
1878	LIB3602-093-Q6-K6-G3	1173194	BLASTX	242	2.00E-23	59	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi 2119093 pir S59594 ribosomal protein S13

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1879	LIB3602-048-Q6-K1QA-H7	1173194	BLASTX	205	5.00E-16	62	precursor, chloroplast - Arabidopsis thaliana >gi 16767 emb CAA79013.1 (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi 662869
1880	LIB3602-055-Q6-K1-C3	6822076	BLASTX	382	9.00E-37	58	30S RIBOSOMAL PROTEIN S13, CHLOROPLAST PRECURSOR (CS13) >gi 2119093 pir S59594 ribosomal protein S13 precursor, chloroplast - Arabidopsis thaliana >gi 16767 emb CAA79013.1 (Z17611) chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi 662869
1881	LIB3602-100-Q1-K1-A11	6822076	BLASTX	322	1.00E-29	50	(AL132957) synaptobrevin-like protein [Arabidopsis thaliana]
1882	LIB3602-083-Q6-K6-H9	7439994	BLASTX	171	8.00E-12	37	glycine-rich RNA-binding protein - garden pea >gi 1778374 gb AAB71417.1 (U81287) glycine-rich RNA-binding protein PsGRBP [Pisum sativum]
1883	LIB3602-109-Q1-K1-H9	7439994	BLASTX	146	7.00E-09	36	glycine-rich RNA-binding protein - garden pea >gi 1778374 gb AAB71417.1 (U81287) glycine-rich RNA-binding protein PsGRBP [Pisum sativum]
1884	LIB3602-043-Q6-K1-F3	6175164	BLASTX	376	6.00E-36	60	(AC011437) putative tryptophanyl-tRNA synthetase [Arabidopsis thaliana]
1885	LIB3602-112-Q1-K1-E4	6175164	BLASTX	148	3.00E-17	42	(AC011437) putative tryptophanyl-tRNA synthetase [Arabidopsis thaliana]
1886	LIB3602-049-Q6-K1-C5	7381225	BLASTX	240	6.00E-20	49	(AF139187) root border cell-specific protein [Pisum sativum]
1887	LIB3602-048-Q6-K1QA-E4	7381225	BLASTX	212	9.00E-17	53	(AF139187) root border cell-specific protein [Pisum sativum]
1888	LIB3602-118-Q1-K1-F9	7492651	BLASTX	154	5.00E-10	83	probable histone h3 variant - fission yeast (Schizosaccharomyces pombe) >gi 5531479 emb CAB50980.1 (AL096851) probable histone h3 variant [Schizosaccharomyces pombe] >gi 7630185 dbj BAA94760.1 (AB041724) CENP-A-like protein SpCENP-A [Schizosaccharomyces]
1889	LIB3602-095-Q6-K6-E8	7492651	BLASTX	149	3.00E-09	80	probable histone h3 variant - fission yeast (Schizosaccharomyces pombe) >gi 5531479 emb CAB50980.1 (AL096851) probable histone h3 variant [Schizosaccharomyces pombe] >gi 7630185 dbj BAA94760.1 (AB041724) CENP-A-like protein SpCENP-A [Schizosaccharomyces]
1890	LIB3602-034-Q6-K1-F8	485512	BLASTX	308	6.00E-28	63	glutathione peroxidase (EC 1.11.1.9) - sweet orange
1891	LIB3602-035-Q1-K1-F8	485512	BLASTX	308	7.00E-28	63	glutathione peroxidase (EC 1.11.1.9) - sweet orange
1892	LIB3602-068-Q1-K1-H7	7438196	BLASTX	243	3.00E-43	74	probable sulfate adenylyltransferase (EC 2.7.7.4) AT51 - Chlamydomonas reinhardtii >gi 1336213 gb AAB01234.1 (U57088) ATP sulfurylase Ats1 [Chlamydomonas reinhardtii]
1893	LIB3602-008-Q6-K1-D8	7438196	BLASTX	418	7.00E-41	60	probable sulfate adenylyltransferase (EC 2.7.7.4) AT51 - Chlamydomonas reinhardtii >gi 1336213 gb AAB01234.1 (U57088) ATP sulfurylase Ats1 [Chlamydomonas reinhardtii]
1894	LIB3602-036-Q6-K1-C10	7451353	BLASTX	683	1.00E-71	75	SAR DNA-binding protein-1 - garden pea >gi 3132696 gb AAC16330.1 (AF061962) SAR DNA-binding protein-1 [Pisum sativum]
1895	LIB3602-058-Q6-K1-G12	7451353	BLASTX	307	3.00E-28	68	SAR DNA-binding protein-1 - garden pea

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1896	LIB3602-017-Q6-K1-F7	6272283	BLASTX	468	1.00E-46	62	>gi 3132696 gb AAC16330.1 (AF061962) SAR DNA-binding protein-1 [Pisum sativum]
1897	LIB3602-101-Q1-K1-H8	6272283	BLASTX	451	9.00E-45	57	(AJ250770) plastidial phosphoglucomutase [Pisum sativum]
1898	LIB3602-081-Q6-K6-G3	4567256	BLASTX	164	2.00E-11	90	(AJ250770) plastidial phosphoglucomutase [Pisum sativum]
1899	LIB3602-082-Q6-K6-B3	4567256	BLASTX	164	2.00E-11	90	(AC007070) 60S ribosomal protein L39 [Arabidopsis thaliana]
1900	LIB3602-047-Q6-K1-E6	401237	BLASTX	489	3.00E-49	60	(AC007070) 60S ribosomal protein L39 [Arabidopsis thaliana]
1901	LIB3602-090-Q6-K6-A1	401237	BLASTX	265	6.00E-23	64	UBIQUITIN-ACTIVATING ENZYME E1 2 >gi 170684 gb AAA34265.1 (M90663) ubiquitin activating enzyme [Triticum aestivum]
1902	LIB3602-039-Q6-K1-A6	1065365	BLASTX	184	3.00E-13	57	UBIQUITIN-ACTIVATING ENZYME E1 2 >gi 170684 gb AAA34265.1 (M90663) ubiquitin activating enzyme [Triticum aestivum]
1903	LIB3602-050-Q6-K1-E8	1065365	BLASTX	180	3.00E-13	54	Alpha-1,4 Glycan-4-Glucanohydrolase (Alpha-Amylase, High Pi Isozyme (Amy2)) (E.C.3.2.1.1) >gi 4699831 pdb 1AVA A Chain A, Amy2BASI PROTEIN-Protein Complex From Barley Seed >gi 4699832 pdb 1AVA B Chain B, Amy2BASI PROTEIN-Protein Complex From Barley Seed >
1904	LIB3602-094-Q6-K6-B2	595775	BLASTX	199	5.00E-15	36	Alpha-1,4 Glycan-4-Glucanohydrolase (Alpha-Amylase, High Pi Isozyme (Amy2)) (E.C.3.2.1.1) >gi 4699831 pdb 1AVA A Chain A, Amy2BASI PROTEIN-Protein Complex From Barley Seed >gi 4699832 pdb 1AVA B Chain B, Amy2BASI PROTEIN-Protein Complex From Barley Seed >
1905	LIB3602-022-Q6-K1-H10	595775	BLASTX	150	1.00E-09	42	(U13869) lacZ alpha peptide [unidentified cloning vector]
1906	LIB3602-065-Q1-K6-C4	6094085	BLASTX	697	2.00E-73	72	(U13869) lacZ alpha peptide [unidentified cloning vector]
1907	LIB3602-080-Q6-K6-H9	6094085	BLASTX	489	4.00E-49	58	60S RIBOSOMAL PROTEIN L5 >gi 7440744 pir T08009 probable ribosomal protein L5 - green alga (Dunaliella salina) >gi 2599104 gb AAB84056.1 (AF028833) 60S ribosomal protein [Dunaliella salina]
1908	LIB3602-018-Q6-K1-C4	4762038	BLASTX	190	5.00E-14	34	60S RIBOSOMAL PROTEIN L5 >gi 7440744 pir T08009 probable ribosomal protein L5 - green alga (Dunaliella salina) >gi 2599104 gb AAB84056.1 (AF028833) 60S ribosomal protein [Dunaliella salina]
1909	LIB3602-049-Q6-K1-D9	4762038	BLASTX	164	4.00E-11	31	(AL031909) probable surface antigen [Leishmania major]
1910	LIB3602-092-Q6-K6-C5	6466950	BLASTX	824	2.00E-88	75	(AL031909) probable surface antigen [Leishmania major]
1911	LIB3602-120-Q1-K1-C5	6466950	BLASTX	329	9.00E-31	72	(AC009176) putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Arabidopsis thaliana] >gi 6648179 gb AAF21177.1 AC013483_1 (AC013483) putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methylt (AC009176) putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I [Arabidopsis thaliana] >gi 6648179 gb AAF21177.1 AC013483_1 (AC013483) putative ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methylt

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1912	LIB3602-057-Q6-K1-D6	129916	BLASTX	350	2.00E-50	51	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi 21835 emb CAA33302.1 (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]
1913	LIB3602-032-Q6-K1-F5	129916	BLASTX	466	2.00E-46	64	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi 66911 pir TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi 21835 emb CAA33302.1 (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]
1914	LIB3602-041-Q6-K1-A5	4586054	BLASTX	320	2.00E-29	41	(AC007020) unknown protein [Arabidopsis thaliana]
1915	LIB3602-013-Q6-K1-H3	4586054	BLASTX	191	2.00E-14	45	(AC007020) unknown protein [Arabidopsis thaliana]
1916	LIB3602-092-Q6-K6-H3	7471624	BLASTX	163	8.00E-11	58	conserved hypothetical protein - Deinococcus radiodurans (strain R1) >gi 6458170 gb AAF10062.1 AE001907_8 (AE001907) conserved hypothetical protein [Deinococcus radiodurans]
1917	LIB3602-113-Q1-K1-H5	7471624	BLASTX	163	8.00E-11	58	conserved hypothetical protein - Deinococcus radiodurans (strain R1) >gi 6458170 gb AAF10062.1 AE001907_8 (AE001907) conserved hypothetical protein [Deinococcus radiodurans]
1918	LIB3602-100-Q1-K1-H1	5734741	BLASTX	434	9.00E-43	54	(AC007651) Similar to Ubiquitin Conjugating Enzyme [Arabidopsis thaliana]
1919	LIB3602-105-Q1-K1-H10	5734741	BLASTX	282	8.00E-25	39	(AC007651) Similar to Ubiquitin Conjugating Enzyme [Arabidopsis thaliana]
1920	LIB3602-036-Q6-K1-H6	7431451	BLASTX	375	1.00E-35	57	rf2 nuclear restorer protein - maize >gi 1421730 gb AAC49371.1 (U43082) RF2 [Zea mays]
1921	LIB3602-030-Q6-K1-H10	7431451	BLASTX	342	5.00E-32	57	rf2 nuclear restorer protein - maize >gi 1421730 gb AAC49371.1 (U43082) RF2 [Zea mays]
1922	LIB3602-043-Q6-K1-C2	7445551	BLASTX	203	2.00E-15	55	ABC-type transport protein T18B16.180 - Arabidopsis thaliana >gi 2828296 emb CAA16710.1 (AL021687) RNase L inhibitor-like protein [Arabidopsis thaliana] >gi 7268716 emb CAB78923.1 (AL161550) RNase L inhibitor-like protein [Arabidopsis thaliana]
1923	LIB3602-061-Q6-K1-B4	7445551	BLASTX	196	7.00E-15	78	ABC-type transport protein T18B16.180 - Arabidopsis thaliana >gi 2828296 emb CAA16710.1 (AL021687) RNase L inhibitor-like protein [Arabidopsis thaliana] >gi 7268716 emb CAB78923.1 (AL161550) RNase L inhibitor-like protein [Arabidopsis thaliana]
1924	LIB3602-070-Q1-K1-C5	6671365	BLASTX	639	1.00E-66	61	(AF216497) P-glycoprotein [Gossypium hirsutum]
1925	LIB3602-021-Q6-K1-C10	6671365	BLASTX	161	4.00E-11	63	(AF216497) P-glycoprotein [Gossypium hirsutum]
1926	LIB3602-063-Q1-K6-F8	7413536	BLASTX	194	2.00E-14	41	(AL162972) putative protein [Arabidopsis thaliana]
1927	LIB3602-072-Q1-K1-G7	7413536	BLASTX	194	2.00E-14	41	(AL162972) putative protein [Arabidopsis thaliana]
1928	LIB3602-087-Q6-K1-E5	7486255	BLASTX	293	4.00E-26	41	hypothetical protein F27G19.20 - Arabidopsis thaliana >gi 4972067 emb CAB43874.1 (AL078467) putative protei [Arabidopsis thaliana] >gi 7269596 emb CAB81392.1 (AL161571) putative protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1929	LIB3602-029-Q6-K1-H2	7486255	BLASTX	221	1.00E-17	32	hypothetical protein F27G19.20 - Arabidopsis thaliana >gi 4972067 emb CAB43874.1 (AL078467) putative protei [Arabidopsis thaliana] >gi 7269596 emb CAB81392.1 (AL161571) putative protein [Arabidopsis thaliana]
1930	LIB3602-109-Q1-K1-C4	3261517	BLASTN	34	3.00E-09	97	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162
1931	LIB3602-083-Q6-K6-C4	3261517	BLASTN	34	4.00E-09	97	Mycobacterium tuberculosis H37Rv complete genome; segment 143/162
1932	LIB3602-052-Q6-K1-E7	6539249	BLASTX	520	7.00E-53	69	(AC011765) geranylgeranyl reductase [Arabidopsis thaliana]
1933	LIB3602-012-Q6-K1-H2	6539249	BLASTX	477	7.00E-48	65	(AC011765) geranylgeranyl reductase [Arabidopsis thaliana]
1934	LIB3602-022-Q6-K1-D9	541954	BLASTX	301	3.00E-27	45	ubiquitin/ribosomal protein S27a fusion protein - white lupine >gi 438111 emb CAA80334.1 (Z22613) ubiquitin extension protein [Lupinus albus]
1935	LIB3602-037-Q6-K1-B12	541954	BLASTX	186	5.00E-14	43	ubiquitin/ribosomal protein S27a fusion protein - white lupine >gi 438111 emb CAA80334.1 (Z22613) ubiquitin extension protein [Lupinus albus]
1936	LIB3602-073-Q1-K1-H5	6091731	BLASTX	489	5.00E-49	48	(AC010797) hypothetical protein [Arabidopsis thaliana]
1937	LIB3602-102-Q1-K1-F5	6091731	BLASTX	408	1.00E-39	48	(AC010797) hypothetical protein [Arabidopsis thaliana]
1938	LIB3602-108-Q1-K1-E3	730652	BLASTX	401	5.00E-55	81	40S RIBOSOMAL PROTEIN S2 (STRINGS OF PEARLS PROTEIN) >gi 1085158 pir S50325 ribosomal protein S2 - fruit fly (Drosophila melanogaster) >gi 515971 gb AAC34198.1 (U01334) ribosomal protein S2 [Drosophila melanogaster] >gi 515972 gb AAA87053.1 (U01335) ri
1939	LIB3602-083-Q6-K6-D3	730652	BLASTX	464	3.00E-46	66	40S RIBOSOMAL PROTEIN S2 (STRINGS OF PEARLS PROTEIN) >gi 1085158 pir S50325 ribosomal protein S2 - fruit fly (Drosophila melanogaster) >gi 515971 gb AAC34198.1 (U01334) ribosomal protein S2 [Drosophila melanogaster] >gi 515972 gb AAA87053.1 (U01335) ri
1940	LIB3602-108-Q1-K1-F7	464705	BLASTX	183	3.00E-15	88	40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal protein S13, cytosolic - maize >gi 288059 emb CAA44311.1 (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]
1941	LIB3602-047-Q6-K1-A5	464705	BLASTX	187	5.00E-14	87	40S RIBOSOMAL PROTEIN S13 >gi 419802 pir S30146 ribosomal protein S13, cytosolic - maize >gi 288059 emb CAA44311.1 (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]
1942	LIB3602-009-Q6-K1-A9	1173055	BLASTX	474	1.00E-47	77	60S RIBOSOMAL PROTEIN L11 (L5) >gi 541961 pir S42497 ribosomal protein L11.e - alfalfa >gi 1076504 pir S51819 ribosomal protein L11, cytosolic - alfalfa >gi 463252 emb CAA55090.1 (X78284) RL5 ribosomal protein [Medicago sativa]
1943	LIB3602-050-Q6-K1-F6	1173055	BLASTX	207	8.00E-17	70	60S RIBOSOMAL PROTEIN L11 (L5) >gi 541961 pir S42497 ribosomal protein L11.e - alfalfa >gi 1076504 pir S51819 ribosomal protein

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1944	LIB3602-006-Q1-K1-G11	567893	BLASTX	208	3.00E-16	43	L11, cytosolic - alfalfa >gi 463252 emb CAA55090.1 (X78284) RL5 ribosomal protein [Medicago sativa]
1945	LIB3602-045-Q6-K1-G10	567893	BLASTX	204	8.00E-16	40	(L37382) beta-galactosidase-complementation protein [unidentified cloning vector]
1946	LIB3602-026-Q6-K1-F10	7469882	BLASTX	181	5.00E-13	40	(L37382) beta-galactosidase-complementation protein [unidentified cloning vector]
1947	LIB3602-042-Q6-K1-H4	7469882	BLASTX	181	5.00E-13	40	hypothetical protein sl0408 - Synechocystis sp. (strain PCC 6803) >gi 1001111 dbj BAA10250.1 (D64001) hypothetical protein [Synechocystis sp.]
1948	LIB3602-072-Q1-K1-G2	7488914	BLASTX	681	1.00E-71	69	hypothetical protein sl0408 - Synechocystis sp. (strain PCC 6803) >gi 1001111 dbj BAA10250.1 (D64001) hypothetical protein [Synechocystis sp.]
1949	LIB3602-065-Q1-K6-G2	7488914	BLASTX	457	2.00E-45	65	embryogenic callus protein 181 - carrot (fragment) >gi 3551247 dbj BAA32822.1 (AB012703) 181 [Daucus carota]
1950	LIB3602-081-Q6-K6-B1	6652882	BLASTX	501	1.00E-50	83	embryogenic callus protein 181 - carrot (fragment) >gi 3551247 dbj BAA32822.1 (AB012703) 181 [Daucus carota]
1951	LIB3602-115-Q1-K1-A4	6652882	BLASTX	326	5.00E-30	77	(AF123392) 26S proteasome AAA-ATPase subunit RPT3 [Arabidopsis thaliana]
1952	LIB3602-070-Q1-K1-H10	7431102	BLASTX	277	3.00E-24	41	(AF123392) 26S proteasome AAA-ATPase subunit RPT3 [Arabidopsis thaliana]
1953	LIB3602-102-Q1-K1-D9	7431102	BLASTX	256	7.00E-22	39	plant metabolite dehydrogenase homolog ytbE - Bacillus subtilis >gi 2293328 gb AAC00406.1 (AF008220) putative morphine dehydrogenase [Bacillus subtilis] >gi 2635370 emb CAB14865.1 (Z99118) similar to plant metabolite dehydrogenase [Bacillus subtilis]
1954	LIB3602-013-Q6-K1-A5	2499807	BLASTX	426	1.00E-41	47	plant metabolite dehydrogenase homolog ytbE - Bacillus subtilis >gi 2293328 gb AAC00406.1 (AF008220) putative morphine dehydrogenase [Bacillus subtilis] >gi 2635370 emb CAB14865.1 (Z99118) similar to plant metabolite dehydrogenase [Bacillus subtilis]
1955	LIB3602-005-Q1-K1-H5	2499807	BLASTX	172	1.00E-12	51	GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK) >gi 7434577 pir S75182 glutamate 5-kinase (EC 2.7.2.11) - Synechocystis sp. (strain PCC 6803) >gi 1652172 dbj BAA17096.1 (D90903) glutamate 5-kinase [Synechocystis sp.]
1956	LIB3602-056-Q6-K1-A2	7487663	BLASTX	152	1.00E-09	34	GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK) >gi 7434577 pir S75182 glutamate 5-kinase (EC 2.7.2.11) - Synechocystis sp. (strain PCC 6803) >gi 1652172 dbj BAA17096.1 (D90903) glutamate 5-kinase [Synechocystis sp.]
1957	LIB3602-039-Q6-K1-F8	7487663	BLASTX	150	2.00E-09	34	hypothetical protein T4L20.280 - Arabidopsis thaliana >gi 3096939 emb CAA18849.1 (AL023094) putative protein [Arabidopsis thaliana] >gi 7270421 emb CAB80187.1 (AL161586) putative protein [Arabidopsis thaliana]
							hypothetical protein T4L20.280 - Arabidopsis thaliana >gi 3096939 emb CAA18849.1 (AL023094) putative protein [Arabidopsis thaliana] >gi 7270421 emb CAB80187.1 (AL161586) putative protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1958	LIB3602-018-Q6-K1-C1	4139215	BLASTN	49	2.00E-18	92	<i>Chlamydomonas reinhardtii</i> light harvesting complex II protein precursor (Lhcb2) mRNA, complete cds
1959	LIB3602-061-Q6-K1-F8	4139215	BLASTN	44	2.00E-15	92	<i>Chlamydomonas reinhardtii</i> light harvesting complex II protein precursor (Lhcb2) mRNA, complete cds
1960	LIB3602-018-Q6-K1-B11	6630729	BLASTX	298	6.00E-27	71	(AL132958) putative protein [<i>Arabidopsis thaliana</i>]
1961	LIB3602-036-Q6-K1-A7	6630729	BLASTX	205	9.00E-16	47	(AL132958) putative protein [<i>Arabidopsis thaliana</i>]
1962	LIB3602-101-Q1-K1-G11	7547401	BLASTX	202	6.00E-30	84	(S66866) cytochrome c1 precursor [<i>Solanum tuberosum</i>]
1963	LIB3602-101-Q1-K1-G6	7547401	BLASTX	154	1.00E-21	72	(S66866) cytochrome c1 precursor [<i>Solanum tuberosum</i>]
1964	LIB3602-070-Q1-K1-B3	7469888	BLASTX	335	5.00E-31	48	hypothetical protein sl0424 - <i>Synechocystis</i> sp. (strain PCC 6803) >gi 1653565 dbj BAA18478.1 (D90914) hypothetical protein [<i>Synechocystis</i> sp.]
1965	LIB3602-081-Q6-K6-F2	7469888	BLASTX	319	3.00E-29	43	hypothetical protein sl0424 - <i>Synechocystis</i> sp. (strain PCC 6803) >gi 1653565 dbj BAA18478.1 (D90914) hypothetical protein [<i>Synechocystis</i> sp.]
1966	LIB3602-061-Q6-K1-G1	7500560	BLASTX	306	1.00E-27	51	hypothetical protein F35G2.2 - <i>Caenorhabditis elegans</i> >gi 3876766 emb CAA93466.1 (Z69637) predicted using Genefinder; Similarity to <i>E.coli</i> hypothetical protein YCAC (SW:YCAC_ECOLI); cDNA EST yk555d12.3 comes from this gene [<i>Caenorhabditis elegans</i>]
1967	LIB3602-026-Q6-K1-B9	7500560	BLASTX	214	5.00E-17	48	hypothetical protein F35G2.2 - <i>Caenorhabditis elegans</i> >gi 3876766 emb CAA93466.1 (Z69637) predicted using Genefinder; Similarity to <i>E.coli</i> hypothetical protein YCAC (SW:YCAC_ECOLI); cDNA EST yk555d12.3 comes from this gene [<i>Caenorhabditis elegans</i>]
1968	LIB3602-063-Q1-K6-H4	7486624	BLASTX	354	3.00E-33	46	hypothetical protein F7N22.3 - <i>Arabidopsis thaliana</i> >gi 3047064 gb AAC13578.1 (AF058825) contains similarity to peptidyl-prolyl cis-trans isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41 [<i>Arabidopsis thaliana</i>])
1969	LIB3602-109-Q1-K1-F2	7486624	BLASTX	329	2.00E-30	58	hypothetical protein F7N22.3 - <i>Arabidopsis thaliana</i> >gi 3047064 gb AAC13578.1 (AF058825) contains similarity to peptidyl-prolyl cis-trans isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41 [<i>Arabidopsis thaliana</i>])
1970	LIB3602-064-Q1-K6-B6	3947719	BLASTX	195	7.00E-15	90	(AJ012653) ribosomal protein S28 [<i>Prunus persica</i>] >gi 3947721 emb CAA10102.1 (AJ012654) ribosomal protein S28 [<i>Prunus persica</i>] >gi 3947723 emb CAA10103.1 (AJ012655) ribosomal protein S28 [<i>Prunus persica</i>]
1971	LIB3602-063-Q1-K6-H5	3947719	BLASTX	191	2.00E-14	97	(AJ012653) ribosomal protein S28 [<i>Prunus persica</i>] >gi 3947721 emb CAA10102.1 (AJ012654) ribosomal protein S28 [<i>Prunus persica</i>] >gi 3947723 emb CAA10103.1 (AJ012655) ribosomal protein S28 [<i>Prunus persica</i>]
1972	LIB3602-010-Q6-K1-C1	5902598	BLASTX	484	1.00E-48	69	(AF110787) light harvesting complex a protein [<i>Volvox carteri</i> f. nagariensis]
1973	LIB3602-077-Q6-K6-B7	5902598	BLASTX	307	1.00E-27	48	(AF110787) light harvesting complex a protein [<i>Volvox carteri</i> f. nagariensis]
1974	LIB3602-068-Q1-K1-C1	549810	BLASTX	575	4.00E-59	70	GTP-BINDING PROTEIN YPTV3 >gi 486945 pir S36366 GTP-binding protein yptV3 - <i>Volvox carteri</i> >gi 409164 gb AAA34252.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1975	LIB3602-060-Q6-K1-A10	549810	BLASTX	402	6.00E-39	69	(L08129) GTP-binding protein [Volvox carteri] GTP-BINDING PROTEIN YPTV3 >gi 486945 pir S36366 GTP-binding protein yptV3 - Volvox carteri >gi 409164 gb AAA34252.1
1976	LIB3602-001-P1-K6-G10	4204304	BLASTX	629	2.00E-65	72	(L08129) GTP-binding protein [Volvox carteri] (AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
1977	LIB3602-021-Q6-K1-A6	4204304	BLASTX	228	6.00E-19	80	(AC003027) lcl prt_seq No definition line found [Arabidopsis thaliana]
1978	LIB3602-089-Q6-K6-A9	6934302	BLASTX	679	2.00E-71	98	(AF221858) polyubiquitin [Euphorbia esula]
1979	LIB3602-032-Q6-K1-F9	6934302	BLASTX	327	2.00E-30	98	(AF221858) polyubiquitin [Euphorbia esula]
1980	LIB3602-052-Q6-K1-B5	115769	BLASTX	301	3.00E-27	54	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB) (LHCP) >gi 81190 pir S00653 chlorophyll a/b-binding protein precursor - Euglena gracilis (fragment) >gi 829262 emb CAA29821.1 (X06602) chlorophyll a/b protein (128 AA) [Euglena gracilis]
1981	LIB3602-022-Q6-K1-H2	115769	BLASTX	274	5.00E-24	55	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I (CAB) (LHCP) >gi 81190 pir S00653 chlorophyll a/b-binding protein precursor - Euglena gracilis (fragment) >gi 829262 emb CAA29821.1 (X06602) chlorophyll a/b protein (128 AA) [Euglena gracilis]
1982	LIB3602-070-Q1-K1-A1	7108521	BLASTX	578	2.00E-59	65	(AF127564) ubiquitin-protein ligase 1 [Arabidopsis thaliana]
1983	LIB3602-067-Q1-K1-H12	7108521	BLASTX	520	5.00E-55	68	(AF127564) ubiquitin-protein ligase 1 [Arabidopsis thaliana]
1984	LIB3602-006-Q1-K1-E6	5739404	BLASTX	173	5.00E-12	40	(AF170026) core subunit of photosystem II precursor [Chlamydomonas reinhardtii]
1985	LIB3602-084-Q6-K1-F7	5739404	BLASTX	156	5.00E-10	33	(AF170026) core subunit of photosystem II precursor [Chlamydomonas reinhardtii]
1986	LIB3602-030-Q6-K1-A11	7486848	BLASTX	383	8.00E-37	60	hypothetical protein T10P11.1 - Arabidopsis thaliana >gi 2262136 gb AAC78251.1 AAC78251 (AC002330) predicted protein of unknown function [Arabidopsis thaliana] >gi 4263520 gb AAD15346.1 (AC004044) predicted protein of unknown function [Arabidopsis thaliana]
1987	LIB3602-063-Q1-K6-E10	7486848	BLASTX	375	8.00E-36	69	hypothetical protein T10P11.1 - Arabidopsis thaliana >gi 2262136 gb AAC78251.1 AAC78251 (AC002330) predicted protein of unknown function [Arabidopsis thaliana] >gi 4263520 gb AAD15346.1 (AC004044) predicted protein of unknown function [Arabidopsis thaliana]
1988	LIB3602-090-Q6-K6-E11	1173218	BLASTX	340	7.00E-32	81	40S RIBOSOMAL PROTEIN S15A >gi 440824 gb AAA61608.1 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi 2150130 gb AAB58750.1 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]
1989	LIB3602-013-Q6-K1-F6	1173218	BLASTX	284	2.00E-25	79	40S RIBOSOMAL PROTEIN S15A >gi 440824 gb AAA61608.1 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi 2150130 gb AAB58750.1 (AF001412) cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
1990	LIB3602-070-Q1-K1-G12	7489195	BLASTX	261	2.00E-22	47	ribosomal protein L10, chloroplast - common tobacco >gi 3298441 dbj BAA31511.1 (AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]
1991	LIB3602-067-Q1-K1-B1	7489195	BLASTX	253	2.00E-21	46	ribosomal protein L10, chloroplast - common tobacco >gi 3298441 dbj BAA31511.1 (AB010879) chloroplast ribosomal protein L10 [Nicotiana tabacum]
1992	LIB3602-016-Q6-K1-F11	7076783	BLASTX	438	3.00E-43	54	(AL132975) methionyl-tRNA synthetase (AtpMetRS) [Arabidopsis thaliana]
1993	LIB3602-072-Q1-K1-B9	7076783	BLASTX	162	2.00E-14	53	(AL132975) methionyl-tRNA synthetase (AtpMetRS) [Arabidopsis thaliana]
1994	LIB3602-014-Q6-K1-G8	586145	BLASTX	605	1.00E-62	69	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 488848 emb CAA55894.1 (X79332) Rieske iron sulphur protein [Solanum tuberosum]
1995	LIB3602-072-Q1-K1-F3	586145	BLASTX	550	3.00E-56	67	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi 488848 emb CAA55894.1 (X79332) Rieske iron sulphur protein [Solanum tuberosum]
1996	LIB3602-094-Q6-K6-A6	7488696	BLASTX	186	1.00E-13	36	polyphosphoinositide binding protein Ssh2 - soybean >gi 2739046 gb AAB94599.1 (AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]
1997	LIB3602-047-Q6-K1-C5	7488696	BLASTX	162	7.00E-11	32	polyphosphoinositide binding protein Ssh2 - soybean >gi 2739046 gb AAB94599.1 (AF024652) polyphosphoinositide binding protein Ssh2p [Glycine max]
1998	LIB3602-114-Q1-K1-B10	4185133	BLASTX	189	7.00E-14	45	(AC005724) putative C3HC4-type RING zinc finger protein [Arabidopsis thaliana]
1999	LIB3602-090-Q6-K6-B10	4185133	BLASTX	185	2.00E-13	45	(AC005724) putative C3HC4-type RING zinc finger protein [Arabidopsis thaliana]
2000	LIB3602-011-Q6-K1-E6	7290666	BLASTX	330	1.00E-30	59	(AE003436) CG5941 gene product [Drosophila melanogaster]
2001	LIB3602-112-Q1-K1-D12	7290666	BLASTX	147	2.00E-09	54	(AE003436) CG5941 gene product [Drosophila melanogaster]
2002	LIB3602-069-Q1-K1-G4	7291506	BLASTX	192	3.00E-14	42	(AE003459) CG3800 gene product [Drosophila melanogaster]
2003	LIB3602-086-Q6-K1-D2	7291506	BLASTX	192	3.00E-14	42	(AE003459) CG3800 gene product [Drosophila melanogaster]
2004	LIB3602-104-Q1-K1-F5	266685	BLASTX	163	7.00E-11	72	DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX (E2) (PDC-E2) (70 KD MITOCHONDRIAL AUTOANTIGEN OF PRIMARY BILIARY CIRRHOSIS) (PBC) >gi 111580 pir S21766 dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - rat (fragment)
2005	LIB3602-104-Q1-K1-H6	266685	BLASTX	163	7.00E-11	72	DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX (E2) (PDC-E2) (70 KD MITOCHONDRIAL AUTOANTIGEN OF PRIMARY BILIARY CIRRHOSIS) (PBC) >gi 111580 pir S21766

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2006	LIB3602-012-Q6-K1-G1	3015514	BLASTX	533	3.00E-54	55	dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) - rat (fragment) (U72351) ADPG pyrophosphorylase small subunit [Arabidopsis thaliana] >gi 7242894 dbj BAA92523.1 (AB039889) glucose-1-phosphate adenylyltransferase [Arabidopsis thaliana]
2007	LIB3602-066-Q1-K6-C1	3015514	BLASTX	522	6.00E-53	55	(U72351) ADPG pyrophosphorylase small subunit [Arabidopsis thaliana] >gi 7242894 dbj BAA92523.1 (AB039889) glucose-1-phosphate adenylyltransferase [Arabidopsis thaliana]
2008	LIB3602-107-Q1-K1-A10	118024	BLASTX	209	2.00E-16	72	CYTOCHROME C >gi 65518 pir CCSP cytochrome c - spinach
2009	LIB3602-120-Q1-K1-G8	118024	BLASTX	204	4.00E-16	82	CYTOCHROME C >gi 65518 pir CCSP cytochrome c - spinach
2010	LIB3602-022-Q6-K1-D5	7299915	BLASTN	45	5.00E-16	89	Drosophila melanogaster genomic scaffold 142000013386035 section 31 of 105, complete sequence
2011	LIB3602-068-Q1-K1-F7	7299915	BLASTN	43	2.00E-14	88	Drosophila melanogaster genomic scaffold 142000013386035 section 31 of 105, complete sequence
2012	LIB3602-083-Q6-K6-A3	7629994	BLASTX	278	8.00E-25	73	(AL132960) 60S RIBOSOMAL PROTEIN L36 homolog [Arabidopsis thaliana]
2013	LIB3602-035-Q1-K1-D7	7629994	BLASTX	252	1.00E-21	71	(AL132960) 60S RIBOSOMAL PROTEIN L36 homolog [Arabidopsis thaliana]
2014	LIB3602-039-Q6-K1-B10	7498202	BLASTX	327	5.00E-30	52	hypothetical protein D2030.5 - Caenorhabditis elegans >gi 3875398 emb CAA98118.1 (Z73906) Similarity to B.subtilis YQJC protein (TR:G1303954); cDNA EST EMBL:T01187 comes from this gene [Caenorhabditis elegans]
2015	LIB3602-004-Q1-K1-B8	7498202	BLASTX	322	2.00E-29	51	hypothetical protein D2030.5 - Caenorhabditis elegans >gi 3875398 emb CAA98118.1 (Z73906) Similarity to B.subtilis YQJC protein (TR:G1303954); cDNA EST EMBL:T01187 comes from this gene [Caenorhabditis elegans]
2016	LIB3602-052-Q6-K1-G1	7492314	BLASTX	303	2.00E-27	51	pop-interacting protein 1 - fission yeast (Schizosaccharomyces pombe) >gi 5853264 gb AAD54393.1 AF179228_1 (AF179228) pop-interacting protein 1 [Schizosaccharomyces pombe] >gi 6073753 emb CAB58559.1 (Z98977) pop-interacting protein 1. [Schizosaccharomyces pombe]
2017	LIB3602-115-Q1-K1-B11	7492314	BLASTX	302	3.00E-27	51	pop-interacting protein 1 - fission yeast (Schizosaccharomyces pombe) >gi 5853264 gb AAD54393.1 AF179228_1 (AF179228) pop-interacting protein 1 [Schizosaccharomyces pombe] >gi 6073753 emb CAB58559.1 (Z98977) pop-interacting protein 1. [Schizosaccharomyces pombe]
2018	LIB3602-022-Q6-K1-C5	6015158	BLASTX	364	1.00E-34	62	FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) >gi 7492278 pir T40724 peptidyl-prolyl cis-trans isomerase - fission yeast (Schizosaccharomyces pombe) >gi 2879879 emb CAA17020.1 (AL021816) peptidyl-prolyl cis-trans isomerase; FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE)
2019	LIB3602-101-Q1-K1-F5	6015158	BLASTX	253	8.00E-28	67	

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2020	LIB3602-107-Q1-K1-A12	2500365	BLASTX	176	2.00E-12	36	>gi 7492278 pir T40724 peptidyl-prolyl cis-trans isomerase - fission yeast (Schizosaccharomyces pombe) >gi 2879879 emb CAA17020.1 (AL021816) peptidyl-prolyl cis-trans isomerase; PROBABLE 60 RIBOSOMAL PROTEIN L14 (HYDROXYPROLINE RICH GLYCOPROTEIN HRGP1)
2021	LIB3602-006-Q1-K1-E4	2500365	BLASTX	171	6.00E-12	38	PROBABLE 60 RIBOSOMAL PROTEIN L14 (HYDROXYPROLINE RICH GLYCOPROTEIN HRGP1)
2022	LIB3602-067-Q1-K1-F3	7485991	BLASTX	282	8.00E-25	44	hypothetical protein F22O13.29 - Arabidopsis thaliana >gi 3063467 gb AAC14055.1 (AC003981) F22O13.29 [Arabidopsis thaliana] >gi 6996317 emb CAB75510.1 (AJ251088) ABI3-interacting protein 3, AIP3 [Arabidopsis thaliana]
2023	LIB3602-084-Q6-K1-H7	7485991	BLASTX	177	2.00E-16	45	hypothetical protein F22O13.29 - Arabidopsis thaliana >gi 3063467 gb AAC14055.1 (AC003981) F22O13.29 [Arabidopsis thaliana] >gi 6996317 emb CAB75510.1 (AJ251088) ABI3-interacting protein 3, AIP3 [Arabidopsis thaliana]
2024	LIB3602-001-P1-K6-H8	585338	BLASTX	755	3.00E-80	72	ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE) >gi 391879 dbj BAA01181.1 (D10335) adenylate kinase-b [Oryza sativa]
2025	LIB3602-037-Q6-K1-D7	585338	BLASTX	376	5.00E-36	64	ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE) >gi 391879 dbj BAA01181.1 (D10335) adenylate kinase-b [Oryza sativa]
2026	LIB3602-118-Q1-K1-D12	7488897	BLASTX	292	5.00E-26	57	hypothetical protein - castor bean >gi 1632831 emb CAA89698.1 (Z49698) orf [Ricinus communis]
2027	LIB3602-084-Q6-K1-A2	7488897	BLASTX	196	6.00E-15	71	hypothetical protein - castor bean >gi 1632831 emb CAA89698.1 (Z49698) orf [Ricinus communis]
2028	LIB3602-045-Q6-K1-F2	7362767	BLASTX	402	5.00E-39	54	(AL162651) 60S RIBOSOMAL PROTEIN L7A protein [Arabidopsis thaliana]
2029	LIB3602-012-Q6-K1-B12	7362767	BLASTX	152	9.00E-10	57	(AL162651) 60S RIBOSOMAL PROTEIN L7A protein [Arabidopsis thaliana]
2030	LIB3602-114-Q1-K1-B1	6006684	BLASTX	247	9.00E-21	44	(AF089106) unknown [Homo sapiens]
2031	LIB3602-088-Q6-K6-D4	6006684	BLASTX	236	2.00E-19	44	(AF089106) unknown [Homo sapiens]
2032	LIB3602-100-Q1-K1-E11	2398681	BLASTX	390	1.00E-37	61	(Y14798) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]
2033	LIB3602-066-Q1-K6-E6	2398681	BLASTX	370	4.00E-35	58	(Y14798) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]
2034	LIB3602-034-Q6-K1-F11	6714302	BLASTX	189	4.00E-14	67	(AC013354) F15H18.8 [Arabidopsis thaliana]
2035	LIB3602-035-Q1-K1-F11	6714302	BLASTX	171	5.00E-12	68	(AC013354) F15H18.8 [Arabidopsis thaliana]
2036	LIB3602-068-Q1-K1-E6	6687300	BLASTN	38	8.00E-12	92	Cyanophora paradoxa partial mRNA for 60S ribosomal protein L7
2037	LIB3602-036-Q6-K1-D10	6687300	BLASTN	33	7.00E-09	93	Cyanophora paradoxa partial mRNA for 60S ribosomal protein L7
2038	LIB3602-106-Q1-K1-G2	3747049	BLASTN	86	3.00E-40	87	Zea mays ribosomal protein L26 mRNA, partial cds
2039	LIB3602-005-Q1-K1-F8	3747049	BLASTN	61	3.00E-25	89	Zea mays ribosomal protein L26 mRNA, partial cds
2040	LIB3602-047-Q6-K1-G12	4507873	BLASTX	280	1.00E-24	40	von Hippel-Lindau binding protein 1 >gi 3212112 emb CAA76761.1 (Y17394) prefoldin subunit 3 [Homo sapiens]
2041	LIB3602-030-Q6-K1-H6	4507873	BLASTX	251	3.00E-21	39	von Hippel-Lindau binding protein 1 >gi 3212112 emb CAA76761.1 (Y17394) prefoldin

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2042	LIB3602-069-Q1-K1-G7	3860277	BLASTX	579	1.00E-59	62	subunit 3 [Homo sapiens] (AC005824) 60S ribosomal protein L10A [Arabidopsis thaliana]
2043	LIB3602-025-Q6-K1-G3	3860277	BLASTX	415	1.00E-40	70	(AC005824) 60S ribosomal protein L10A [Arabidopsis thaliana]
2044	LIB3602-011-Q6-K1-C8	2499932	BLASTX	298	9.00E-27	59	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi 7433931 pir T06263 adenine phosphoribosyltransferase (EC 2.4.2.7) APT1 - wheat >gi 726305 gb AAA80609.1 (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]
2045	LIB3602-084-Q6-K1-G3	2499932	BLASTX	166	9.00E-20	66	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi 7433931 pir T06263 adenine phosphoribosyltransferase (EC 2.4.2.7) APT1 - wheat >gi 726305 gb AAA80609.1 (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]
2046	LIB3602-114-Q1-K1-F11	7487365	BLASTX	408	1.00E-39	57	hypothetical protein T23J7.140 - Arabidopsis thaliana >gi 4741198 emb CAB41864.1 (AL049746) putative protein [Arabidopsis thaliana]
2047	LIB3602-118-Q1-K1-G2	7487365	BLASTX	286	1.00E-35	60	hypothetical protein T23J7.140 - Arabidopsis thaliana >gi 4741198 emb CAB41864.1 (AL049746) putative protein [Arabidopsis thaliana]
2048	LIB3602-013-Q6-K1-B4	3387899	BLASTX	789	2.00E-84	88	(AF070540) putative nuclear protein [Homo sapiens]
2049	LIB3602-087-Q6-K1-G7	3387899	BLASTX	597	9.00E-62	67	(AF070540) putative nuclear protein [Homo sapiens]
2050	LIB3602-010-Q6-K1-F11	464621	BLASTX	465	2.00E-46	64	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586 ribosomal protein ML16, cytosolic - common ice plant >gi 19539 emb CAA49175.1 (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]
2051	LIB3602-039-Q6-K1-G8	464621	BLASTX	433	1.00E-42	65	60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586 ribosomal protein ML16, cytosolic - common ice plant >gi 19539 emb CAA49175.1 (X69378) ribosomal protein YL16 [Mesembryanthemum crystallinum]
2052	LIB3602-058-Q6-K1-E4	6446570	BLASTX	449	2.00E-44	71	(AU066541) hypothetical protein [Chlamydomonas sp.]
2053	LIB3602-046-Q6-K1-G7	6446570	BLASTX	446	3.00E-44	70	(AU066541) hypothetical protein [Chlamydomonas sp.]
2054	LIB3602-042-Q6-K1-E3	7445817	BLASTX	356	2.00E-33	59	ABC-type transport protein slr0864 - Synechocystis sp. (strain PCC 6803) >gi 1652892 dbj BAA17810.1 (D90909) ABC transporter [Synechocystis sp.]
2055	LIB3602-003-Q1-K1-C4	7445817	BLASTX	332	9.00E-31	61	ABC-type transport protein slr0864 - Synechocystis sp. (strain PCC 6803) >gi 1652892 dbj BAA17810.1 (D90909) ABC transporter [Synechocystis sp.]
2056	LIB3602-118-Q1-K1-E9	18163	BLASTN	39	3.00E-12	85	C.reinhardtii psb3 mRNA for OEE3 protein of photosystem II (oxygen-evolving protein)
2057	LIB3602-035-Q1-K1-E4	18163	BLASTN	37	6.00E-11	97	C.reinhardtii psb3 mRNA for OEE3 protein of photosystem II (oxygen-evolving protein)
2058	LIB3602-065-Q1-K6-F12	1361925	BLASTX	283	6.00E-25	36	translation elongation factor aEF-1 alpha chain - Desulfurococcus mobilis
2059	LIB3602-071-Q1-K1-B5	1361925	BLASTX	257	7.00E-22	37	translation elongation factor aEF-1 alpha chain - Desulfurococcus mobilis

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2060	LIB3602-026-Q6-K1-C9	5442410	BLASTX	304	1.00E-32	52	(AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
2061	LIB3602-005-Q1-K1-G1	5442410	BLASTX	298	9.00E-27	41	(AF159254) ascorbate peroxidase [Zantedeschia aethiopica]
2062	LIB3602-029-Q6-K1-B12	2739219	BLASTX	248	5.00E-21	92	(AJ001161) rpS28 [Hordeum vulgare]
2063	LIB3602-030-Q6-K1-F5	2739219	BLASTX	248	5.00E-21	92	(AJ001161) rpS28 [Hordeum vulgare]
2064	LIB3602-090-Q6-K6-C8	6633821	BLASTX	180	7.00E-13	39	(AC009519) FIN19.23 [Arabidopsis thaliana]
2065	LIB3602-091-Q6-K6-C8	6633821	BLASTX	180	7.00E-13	39	(AC009519) FIN19.23 [Arabidopsis thaliana]
2066	LIB3602-001-P1-K6-B1	6320203	BLASTX	262	2.00E-22	38	Ydl001wp >gi 1077511 pir S50981 probable membrane protein YDL001w - yeast (Saccharomyces cerevisiae) >gi 642805 emb CAA88060.1 (Z48008) unknown [Saccharomyces cerevisiae]
2067	LIB3602-002-P1-K6-C4	6320203	BLASTX	194	1.00E-14	34	Ydl001wp >gi 1077511 pir S50981 probable membrane protein YDL001w - yeast (Saccharomyces cerevisiae) >gi 642805 emb CAA88060.1 (Z48008) unknown [Saccharomyces cerevisiae]
2068	LIB3602-065-Q1-K6-D12	7488076	BLASTX	532	3.00E-54	67	probable clathrin-associated protein F23E12.30 - Arabidopsis thaliana >gi 2231702 gb AAB96889.1 (U92086) clathrin assembly protein AP19 homolog [Arabidopsis thaliana] >gi 3080409 emb CAA18728.1 (AL022604) clathrin assembly protein AP19 homolog [Arabidopsis thaliana]
2069	LIB3602-004-Q1-K1-H1	7488076	BLASTX	190	4.00E-14	64	probable clathrin-associated protein F23E12.30 - Arabidopsis thaliana >gi 2231702 gb AAB96889.1 (U92086) clathrin assembly protein AP19 homolog [Arabidopsis thaliana] >gi 3080409 emb CAA18728.1 (AL022604) clathrin assembly protein AP19 homolog [Arabidopsis thaliana]
2070	LIB3602-070-Q1-K1-F10	6321354	BLASTX	430	4.00E-42	43	Ygl084cp >gi 1723878 sp P53154 YGI4_YEAST HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION >gi 2132541 pir S64091 probable membrane protein YGL084c - yeast (Saccharomyces cerevisiae) >gi 1322607 emb CAA96789.1 (Z72606) ORF YGL084c [Saccharomyces cerevisiae]
2071	LIB3602-054-Q6-K1-E2	6321354	BLASTX	209	2.00E-16	35	Ygl084cp >gi 1723878 sp P53154 YGI4_YEAST HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION >gi 2132541 pir S64091 probable membrane protein YGL084c - yeast (Saccharomyces cerevisiae) >gi 1322607 emb CAA96789.1 (Z72606) ORF YGL084c [Saccharomyces cerevisiae]
2072	LIB3602-062-Q6-K1-H5	1707012	BLASTX	692	6.00E-73	72	(U78721) putative tyrosyl-tRNA synthetase [Arabidopsis thaliana]
2073	LIB3602-062-Q6-K1-H6	1707012	BLASTX	301	5.00E-27	64	(U78721) putative tyrosyl-tRNA synthetase [Arabidopsis thaliana]
2074	LIB3602-107-Q1-K1-H1	7543908	BLASTX	600	4.00E-62	66	(AL163572) putative protein [Arabidopsis thaliana]
2075	LIB3602-079-Q6-K6-H1	7543908	BLASTX	236	2.00E-19	75	(AL163572) putative protein [Arabidopsis thaliana]
2076	LIB3602-089-Q6-K6-E6	1170507	BLASTX	550	3.00E-56	92	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi 100276 pir S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi 19699 emb CAA43514.1 (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2077	LIB3602-118-Q1-K1-H8	1170507	BLASTX	403	7.00E-55	95	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi 100276 pir S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi 19699 emb CAA43514.1 (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]
2078	LIB3602-010-Q6-K1-G3	7378766	BLASTX	704	2.00E-74	75	(AJ277097) putative kinetochore protein [Hordeum vulgare]
2079	LIB3602-100-Q1-K1-B6	7378766	BLASTX	575	3.00E-59	72	(AJ277097) putative kinetochore protein [Hordeum vulgare]
2080	LIB3602-100-Q1-K1-C6	3881976	BLASTX	173	3.00E-24	74	(AJ012409) hypothetical protein [Homo sapiens]
2081	LIB3602-108-Q1-K1-C6	3881976	BLASTX	162	4.00E-23	70	(AJ012409) hypothetical protein [Homo sapiens]
2082	LIB3602-065-Q1-K6-D11	5817608	BLASTX	349	8.00E-33	46	(AF137288) putative translation initiation factor 2B beta subunit [Nicotiana tabacum]
2083	LIB3602-111-Q1-K1-H6	5817608	BLASTX	197	2.00E-15	45	(AF137288) putative translation initiation factor 2B beta subunit [Nicotiana tabacum]
2084	LIB3602-100-Q1-K1-C8	7431833	BLASTX	308	7.00E-44	67	NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor, mitochondrial - human >gi 1110520 gb AAC51914.1 (U40490) nicotinamide nucleotide transhydrogenase [Homo sapiens]
2085	LIB3602-001-P1-K6-A11	7431833	BLASTX	245	2.00E-20	67	NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor, mitochondrial - human >gi 1110520 gb AAC51914.1 (U40490) nicotinamide nucleotide transhydrogenase [Homo sapiens]
2086	LIB3602-067-Q1-K1-G4	465847	BLASTX	697	2.00E-73	67	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi 280542 pir S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans >gi 3875448 emb CAA79618.1 (Z19555) predicted using Genefinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST
2087	LIB3602-104-Q1-K1-F2	465847	BLASTX	141	4.00E-09	66	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi 280542 pir S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans >gi 3875448 emb CAA79618.1 (Z19555) predicted using Genefinder; similar to Propionyl-CoA carboxylase beta chain; cDNA EST
2088	LIB3602-086-Q6-K1-F2	7469487	BLASTX	178	1.00E-12	37	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1653572 dbj BAA18485.1 (D90914) sterol-C-methyltransferase [Synechocystis sp.]
2089	LIB3602-067-Q1-K1-E12	7469487	BLASTX	177	2.00E-12	42	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1653572 dbj BAA18485.1 (D90914) sterol-C-methyltransferase [Synechocystis sp.]
2090	LIB3602-022-Q6-K1-F3	266947	BLASTX	225	3.00E-18	47	60S ACIDIC RIBOSOMAL PROTEIN P1 >gi 71168 pir R6KM1C acidic ribosomal protein P1, cytosolic - Chlamydomonas reinhardtii >gi 18211 emb CAA47042.1 (X66411) ribosomal protein P1 [Chlamydomonas reinhardtii]
2091	LIB3602-042-Q6-K1-F8	266947	BLASTX	148	3.00E-09	40	60S ACIDIC RIBOSOMAL PROTEIN P1 >gi 71168 pir R6KM1C acidic ribosomal protein P1, cytosolic - Chlamydomonas reinhardtii >gi 18211 emb CAA47042.1 (X66411) ribosomal protein P1 [Chlamydomonas reinhardtii]
2092	LIB3602-069-Q1-K1-E7	4218951	BLASTX	399	2.00E-38	80	(AF081796) fructose-1,6-bisphosphatase precursor [Brassica napus]
2093	LIB3602-086-Q6-K1-F3	4218951	BLASTX	210	2.00E-16	65	(AF081796) fructose-1,6-bisphosphatase precursor

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2094	LIB3602-041-Q6-K1-C4	6815060	BLASTX	894	1.00E-96	96	[Brassica napus] (AP001080) EST C26994(C50622) corresponds to a region of the predicted gene.; Similar to ADP-ribosylation factor. (D17760) [Oryza sativa] >gi 7242921 dbj BAA92519.1 (AP001383) EST C26994(C50622) corresponds to a region of the predicted gene.; Similar to
2095	LIB3602-058-Q6-K1-B8	6815060	BLASTX	634	3.00E-66	97	(AP001080) EST C26994(C50622) corresponds to a region of the predicted gene.; Similar to ADP-ribosylation factor. (D17760) [Oryza sativa] >gi 7242921 dbj BAA92519.1 (AP001383) EST C26994(C50622) corresponds to a region of the predicted gene.; Similar to
2096	LIB3602-060-Q6-K1-G3	4138855	BLASTX	489	4.00E-49	54	(AF098072) IMMUTANS [Arabidopsis thaliana]
2097	LIB3602-017-Q6-K1-C2	4138855	BLASTX	475	2.00E-47	53	(AF098072) IMMUTANS [Arabidopsis thaliana]
2098	LIB3602-112-Q1-K1-A4	4759280	BLASTX	194	1.00E-14	68	U5 snRNP-specific protein, 116 kD >gi 434759 dbj BAA04699.1 (D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]
2099	LIB3602-089-Q6-K6-A4	4759280	BLASTX	190	5.00E-14	66	U5 snRNP-specific protein, 116 kD >gi 434759 dbj BAA04699.1 (D21163) similar to human elongation factor 2 mRNA (HSEF2). [Homo sapiens]
2100	LIB3602-074-Q1-K1-E1	3687251	BLASTX	183	2.00E-13	42	(AC005169) putative ribosomal protein L28 [Arabidopsis thaliana]
2101	LIB3602-087-Q6-K1-A2	3687251	BLASTX	177	1.00E-12	40	(AC005169) putative ribosomal protein L28 [Arabidopsis thaliana]
2102	LIB3602-050-Q6-K1-C2	7489246	BLASTX	374	9.00E-36	55	oxoglutarate/malate translocator - potato >gi 1486472 emb CAA68164.1 (X99853) oxoglutarate malate translocator [Solanum tuberosum]
2103	LIB3602-063-Q1-K6-D5	7489246	BLASTX	357	1.00E-33	49	oxoglutarate/malate translocator - potato >gi 1486472 emb CAA68164.1 (X99853) oxoglutarate malate translocator [Solanum tuberosum]
2104	LIB3602-012-Q6-K1-A12	7435806	BLASTX	356	2.00E-33	48	cysteine proteinase mir3 (EC 3.4.22.-) - maize >gi 2425066 gb AAB88263.1 (AF019147) cysteine proteinase Mir3 [Zea mays]
2105	LIB3602-036-Q6-K1-F11	7435806	BLASTX	255	1.00E-21	42	cysteine proteinase mir3 (EC 3.4.22.-) - maize >gi 2425066 gb AAB88263.1 (AF019147) cysteine proteinase Mir3 [Zea mays]
2106	LIB3602-064-Q1-K6-B11	3334112	BLASTX	279	2.00E-24	60	ACYL-COA-BINDING PROTEIN (ACBP) >gi 7441625 pir T09844 acyl-CoA-binding protein - castor bean >gi 1938236 emb CAA70200.1 (Y08996) acyl-CoA-binding protein [Ricinus communis]
2107	LIB3602-011-Q6-K1-H5	3334112	BLASTX	278	2.00E-24	60	ACYL-COA-BINDING PROTEIN (ACBP) >gi 7441625 pir T09844 acyl-CoA-binding protein - castor bean >gi 1938236 emb CAA70200.1 (Y08996) acyl-CoA-binding protein [Ricinus communis]
2108	LIB3602-078-Q6-K6-F9	6498428	BLASTX	684	6.00E-72	69	(AP000815) Similar to Arabidopsis thaliana chromosome II BAC T27A16 sequence; hypothetical protein. (AC005496) [Oryza sativa]
2109	LIB3602-072-Q1-K1-E5	6498428	BLASTX	648	1.00E-67	68	(AP000815) Similar to Arabidopsis thaliana chromosome II BAC T27A16 sequence; hypothetical protein. (AC005496) [Oryza sativa]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2110	LIB3602-041-Q6-K1-A4	7549645	BLASTX	199	1.00E-15	82	(AC023912) ribosomal protein L29, putative [Arabidopsis thaliana]
2111	LIB3602-010-Q6-K1-H9	7549645	BLASTX	199	2.00E-15	82	(AC023912) ribosomal protein L29, putative [Arabidopsis thaliana]
2112	LIB3602-074-Q1-K1-C9	3153873	BLASTX	829	6.00E-89	77	(AF065393) putative G-binding protein [Homo sapiens]
2113	LIB3602-107-Q1-K1-B12	3153873	BLASTX	773	2.00E-82	79	(AF065393) putative G-binding protein [Homo sapiens]
2114	LIB3602-027-Q6-K1-A6	7271018	BLASTX	274	5.00E-24	54	(AJ390506) ribosomal protein L16 [Candida albicans]
2115	LIB3602-049-Q6-K1-C12	7271018	BLASTX	202	1.00E-15	50	(AJ390506) ribosomal protein L16 [Candida albicans]
2116	LIB3602-041-Q6-K1-A3	7469371	BLASTX	654	2.00E-68	60	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1001311 dbj BAA10798.1 (D64006) hypothetical protein [Synechocystis sp.]
2117	LIB3602-041-Q6-K1-A8	7469371	BLASTX	199	4.00E-15	52	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1001311 dbj BAA10798.1 (D64006) hypothetical protein [Synechocystis sp.]
2118	LIB3602-091-Q6-K6-B11	7484843	BLASTX	397	3.00E-38	66	cell division protein ftsY homolog F4I18.25 - Arabidopsis thaliana >gi 3386617 gb AAC28547.1 (AC004665) putative signal recognition particle receptor (alpha subunit) [Arabidopsis thaliana]
2119	LIB3602-094-Q6-K6-B11	7484843	BLASTX	285	3.00E-25	54	cell division protein ftsY homolog F4I18.25 - Arabidopsis thaliana >gi 3386617 gb AAC28547.1 (AC004665) putative signal recognition particle receptor (alpha subunit) [Arabidopsis thaliana]
2120	LIB3602-093-Q6-K6-H4	729396	BLASTX	278	2.00E-24	36	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (ELONGATION FACTOR TU) (EF-TU) >gi 581023 emb CAA51984.1 (X73582) elongation factor 1-alpha [Desulfurococcus mobilis]
2121	LIB3602-101-Q1-K1-C3	729396	BLASTX	226	2.00E-18	37	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (ELONGATION FACTOR TU) (EF-TU) >gi 581023 emb CAA51984.1 (X73582) elongation factor 1-alpha [Desulfurococcus mobilis]
2122	LIB3602-038-Q6-K1-D11	2494208	BLASTX	265	5.00E-23	58	DYNEIN BETA CHAIN, FLAGELLAR OUTER ARM >gi 7484362 pir T08030 dynein beta heavy chain - Chlamydomonas reinhardtii >gi 514215 gb AAA19956.1 (U02963) dynein beta heavy chain [Chlamydomonas reinhardtii]
2123	LIB3602-038-Q6-K1-D12	2494208	BLASTX	153	5.00E-10	40	DYNEIN BETA CHAIN, FLAGELLAR OUTER ARM >gi 7484362 pir T08030 dynein beta heavy chain - Chlamydomonas reinhardtii >gi 514215 gb AAA19956.1 (U02963) dynein beta heavy chain [Chlamydomonas reinhardtii]
2124	LIB3602-072-Q1-K1-D11	4836948	BLASTX	526	2.00E-53	64	(AC006085) Similar to human CGI-33 protein [Arabidopsis thaliana]
2125	LIB3602-028-Q6-K1-B7	4836948	BLASTX	367	7.00E-35	63	(AC006085) Similar to human CGI-33 protein [Arabidopsis thaliana]
2126	LIB3602-047-Q6-K1-F2	3023740	BLASTX	367	7.00E-35	75	FERREDOXIN >gi 7430737 pir A68399 ferredoxin [2Fe-2S] - Chlorella fusca >gi 2914662 pdb 1AWD Ferredoxin [2fe-2s] Oxidized Form From Chlorella Fusca
2127	LIB3602-029-Q6-K1-A12	3023740	BLASTX	340	9.00E-32	82	FERREDOXIN >gi 7430737 pir A68399 ferredoxin [2Fe-2S] - Chlorella fusca >gi 2914662 pdb 1AWD Ferredoxin [2fe-2s] Oxidized Form From Chlorella Fusca
2128	LIB3602-003-Q1-K1-D5	417744	BLASTX	635	3.00E-66	74	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							HYDROLASE) (ADOH CYASE) >gi 169663 gb AAA33856.1 (M81885) S-adenosylhomocysteine hydrolase [Petroselinum crispum]
2129	LIB3602-115-Q1-K1-G10	417744	BLASTX	492	7.00E-62	71	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOH CYASE) >gi 169663 gb AAA33856.1 (M81885) S-adenosylhomocysteine hydrolase [Petroselinum crispum]
2130	LIB3602-064-Q1-K6-E11	1172811	BLASTX	479	4.00E-48	89	60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPPRESSOR SC34) >gi 1076751 pir S49575 ribosomal protein L10.e, cytosolic - rice >gi 575355 emb CAA57339.1 (X81691) putative tumor suppresser [Oryza sativa]
2131	LIB3602-117-Q1-K1-E9	1172811	BLASTX	195	1.00E-27	87	60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPPRESSOR SC34) >gi 1076751 pir S49575 ribosomal protein L10.e, cytosolic - rice >gi 575355 emb CAA57339.1 (X81691) putative tumor suppresser [Oryza sativa]
2132	LIB3602-040-Q6-K1-B11	6319773	BLASTX	235	2.00E-19	36	Probable Na ⁺ /Pi symporter; Pho89p >gi 586363 sp P38361 YB8I_YEAST PUTATIVE PHOSPHATE-REPRESSIBLE PHOSPHATE PERMEASE YBR29C >gi 626777 pir S46178 phosphate-repressible phosphate permease homolog YBR296c - yeast (Saccharomyces cerevisiae) >gi 536756 emb CA
2133	LIB3602-053-Q6-K1-H12	6319773	BLASTX	221	6.00E-18	36	Probable Na ⁺ /Pi symporter; Pho89p >gi 586363 sp P38361 YB8I_YEAST PUTATIVE PHOSPHATE-REPRESSIBLE PHOSPHATE PERMEASE YBR29C >gi 626777 pir S46178 phosphate-repressible phosphate permease homolog YBR296c - yeast (Saccharomyces cerevisiae) >gi 536756 emb CA
2134	LIB3602-106-Q1-K1-F10	7322532	BLASTX	206	7.00E-16	45	(AC024756) contains similarity to SW:GLRX_RABIT [Caenorhabditis elegans]
2135	LIB3602-100-Q1-K1-F10	7322532	BLASTX	205	7.00E-16	46	(AC024756) contains similarity to SW:GLRX_RABIT [Caenorhabditis elegans]
2136	LIB3602-047-Q6-K1-C6	5714433	BLASTX	325	5.00E-30	41	(AF120112) chloroplast SRP receptor homolog, alpha subunit CPFTSY; chloroplast signal recognition particle receptor alpha homolog CPFTSY [Arabidopsis thaliana]
2137	LIB3602-066-Q1-K6-E3	5714433	BLASTX	202	2.00E-15	44	(AF120112) chloroplast SRP receptor homolog, alpha subunit CPFTSY; chloroplast signal recognition particle receptor alpha homolog CPFTSY [Arabidopsis thaliana]
2138	LIB3602-047-Q6-K1-F4	6644196	BLASTX	193	2.00E-14	86	(AF207690) chlorophyll a/b-binding protein [Daucus carota]
2139	LIB3602-059-Q6-K1-H9	6644196	BLASTX	193	2.00E-14	86	(AF207690) chlorophyll a/b-binding protein [Daucus carota]
2140	LIB3602-065-Q1-K6-H11	4835754	BLASTX	624	6.00E-65	76	(AC007202) Is a member of the PF00162 Phosphoglycerate kinase family. ESTs gb N38721, gb T22178, gb R90345, gb R90715, gb T21140, gb T46295, gb H37082, gb T46076, gb N37132, gb AA597649, gb A1100648 and gb Z48462 come from this gene. [Arabidopsis tha>
2141	LIB3602-057-Q6-K1-F2	4835754	BLASTX	542	2.00E-55	67	(AC007202) Is a member of the PF00162 Phosphoglycerate kinase family. ESTs gb N38721,

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							gb T22178, gb R90345, gb R90715, gb T21140, gb T46295, gb H37082, gb T46076, gb N37132, gb AA597649, gb AI100648 and gb Z48462 come from this gene. [Arabidopsis tha>
2142	LIB3602-083-Q6-K6-E4	7385201	BLASTX	632	8.00E-66	70	(AF243182) beta-ketoacyl-ACP synthetase I [Glycine max]
2143	LIB3602-062-Q6-K1-E3	7331195	BLASTX	149	3.00E-09	33	(AF236108) putative purple acid phosphatase precursor [Glycine max]
2144	LIB3602-068-Q1-K1-H1	5441551	BLASTX	362	2.00E-34	63	(AJ388528) Ribosomal protein [Canis familiaris]
2145	LIB3602-063-Q1-K6-A2	7300833	BLASTX	314	1.00E-28	37	(AE003738) CG5383 gene product [Drosophila melanogaster]
2146	LIB3602-038-Q6-K1-F5	7487011	BLASTX	193	2.00E-14	36	hypothetical protein T14P8.20 - Arabidopsis thaliana >gi 3193300 gb AAC19284.1 (AF069298) T14P8.20 gene product [Arabidopsis thaliana] >gi 7269000 emb CAB80733.1 (AL161494) contains EST gb:AI998867.1 [Arabidopsis thaliana] (AF130441) UVB-resistance protein UVR8 [Arabidopsis thaliana]
2147	LIB3602-042-Q6-K1-E7	5478530	BLASTX	261	2.00E-22	40	(AF130845) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]
2148	LIB3602-074-Q1-K1-A11	7108615	BLASTX	380	4.00E-41	63	(AF130845) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]
2149	LIB3602-086-Q6-K1-G7	6912654	BLASTX	456	3.00E-45	56	splicing factor 3b, subunit 1, 155kd >gi 4033735 gb AAC97189.1 (AF054284) spliceosomal protein SAP 155 [Homo sapiens]
2150	LIB3602-104-Q1-K1-G1	477724	BLASTX	221	1.00E-17	73	acetyl-CoA synthetase homolog - Escherichia coli (fragment) >gi 148105 gb AAA24715.1 (M87509) acetyl-CoA synthetase [Escherichia coli]
2151	LIB3602-051-Q6-K1-B3	4874275	BLASTX	403	4.00E-39	53	(AC007354) Similar to gb L26291 clathrin-associated protein unc-101 from Caenorhabditis elegans and is a member of the PF 00928 Adapter complexes medium subunit family. [Arabidopsis thaliana]
2152	LIB3602-086-Q6-K1-A12	7485223	BLASTX	309	5.00E-28	62	hypothetical protein A_IG002N01.18 - Arabidopsis thaliana >gi 2191138 gb AAB61025.1 (AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana] >gi 7267612 emb CAB80924.1 (AL161491) hypothetical protein [Arabidopsis thaliana]
2153	LIB3602-015-Q6-K1-F6	5729802	BLASTX	601	3.00E-62	87	similar to S. pombe dim1+ >gi 6225270 sp O14834 DIM1_HUMAN DIM1 PROTEIN HOMOLOG >gi 6730460 pdb 1QGV A Chain A, Human Spliceosomal Protein U5-15kd >gi 2565275 gb AAB81950.1 (AF023611) Dim1p homolog [Homo sapiens] >gi 6572636 gb AAF17332.1 AF146373_1 (AF1
2154	LIB3602-045-Q6-K1-H6	4506729	BLASTX	162	4.00E-11	35	ribosomal protein S5 >gi 1173267 sp P46782 RS5_HUMAN 40S RIBOSOMAL PROTEIN S5 >gi 1362935 pir S55916 ribosomal protein S5, cytosolic - human >gi 550021 gb AAA85658.1 (U14970) ribosomal protein S5 [Homo sapiens] >gi 1096942 prf 2113200E ribosomal protei
2155	LIB3602-020-Q6-K1-C11	6681153	BLASTX	255	9.00E-22	50	dolichyl-di-phosphooligosaccharide-protein glycotransferase >gi 2662377 dbj BAA23671.1 (D89063) oligosaccharyltransferase [Mus musculus] (AC009853) unknown protein [Arabidopsis thaliana]
2156	LIB3602-023-Q6-K1-A4	6041851	BLASTX	155	6.00E-10	56	(AC009853) unknown protein [Arabidopsis thaliana]
2157	LIB3602-006-Q1-K1-F8	7293667	BLASTX	232	7.00E-19	40	(AE003514) CG6597 gene product [Drosophila

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2158	LIB3602-019-Q6-K1-C11	6652878	BLASTX	645	1.00E-67	92	melanogaster] (AF123390) 26S proteasome AAA-ATPase subunit RPT1a [Arabidopsis thaliana]
2159	LIB3602-076-Q6-K6-B2	6322518	BLASTX	197	6.00E-15	59	Clathrin-associated protein, small subunit; Aps2p >gi 231554 sp Q00381 AP17_YEAST CLATHRIN COAT ASSEMBLY PROTEIN AP17 (CLATHRIN COAT ASSOCIATED PROTEIN AP17) (PLASMA MEMBRANE ADAPTOR AP-2 17 KD PROTEIN) (HA2 17 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN 2 SMA
2160	LIB3602-001-P1-K6-E2	2497984	BLASTX	218	3.00E-17	31	MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER PROTEIN (CARNITINE/ACYLCARNITINE TRANSLOCASE) (CAC) >gi 1842211 emb CAA66410.1 (X97831) carnitine/acylcarnitine carrier protein [Rattus norvegicus]
2161	LIB3602-089-Q6-K6-B2	7025513	BLASTX	167	2.00E-11	54	(AF233593) ascorbate oxidase AO1 [Cucumis melo]
2162	LIB3602-101-Q1-K1-G1	6840800	BLASTX	247	1.00E-30	60	ADENOSINE KINASE (AK) (ADENOSINE 5'-PHOSPHOTRANSFERASE)
2163	LIB3602-077-Q6-K6-A5	6525009	BLASTX	169	1.00E-11	46	(AF198626) copper chaperone homolog CCH [Oryza sativa]
2164	LIB3602-077-Q6-K6-G5	4836473	BLASTX	218	3.00E-17	45	(AF123257) 17.6 kD class I small heat shock protein [Lycopersicon esculentum]
2165	LIB3602-038-Q6-K1-F6	7340070	BLASTX	412	9.00E-45	70	(AF220552) ribosomal protein L17 [Paralichthys olivaceus]
2166	LIB3602-050-Q6-K1-C5	6735351	BLASTX	433	1.00E-42	57	(AL137081) pelota-like protein [Arabidopsis thaliana]
2167	LIB3602-003-Q1-K1-E7	7302653	BLASTX	191	3.00E-14	52	(AE003800) Dgp-1 gene product [Drosophila melanogaster]
2168	LIB3602-090-Q6-K6-F9	6325229	BLASTX	204	1.00E-15	54	acetoacetyl CoA thiolase; Erg10p >gi 730943 sp P41338 THIL_YEAST ACETYL-COA ACETYLTRANSFERASE (ACETOACETYL-COA THIOLASE) >gi 1071833 pir A55654 acetyl-CoA C-acetyltransferase (EC 2.3.1.9), cytosolic - yeast (Saccharomyces cerevisiae) >gi 311089 gb AAA623
2169	LIB3602-087-Q6-K1-B6	2500430	BLASTX	467	6.00E-49	70	40S RIBOSOMAL PROTEIN S16
2170	LIB3602-051-Q6-K1-D4	7437805	BLASTX	602	5.00E-68	77	phenylalanine-tRNA ligase homolog T22F8.180 - Arabidopsis thaliana >gi 4914440 emb CAB43643.1 (AL050351) phenylalanyl-trna synthetase-like protein [Arabidopsis thaliana] >gi 7270911 emb CAB80591.1 (AL161594) phenylalanyl-trna synthetase-like protein [Ar
2171	LIB3602-028-Q6-K1-B3	5923675	BLASTX	347	2.00E-32	42	(AC009326) putative mRNA capping enzyme, RNA guanylyltransferase [Arabidopsis thaliana]
2172	LIB3602-029-Q6-K1-B2	7491269	BLASTX	149	3.00E-09	44	hypothetical protein SPAC8C9.11 - fission yeast (Schizosaccharomyces pombe) >gi 2408094 emb CAB16299.1 (Z99168) hypothetical protein [Schizosaccharomyces pombe]
2173	LIB3602-068-Q1-K1-B11	7267629	BLASTX	229	9.00E-19	54	(AL161491) putative CAAX prenyl protease [Arabidopsis thaliana]
2174	LIB3602-066-Q1-K6-H9	4558669	BLASTX	328	4.00E-30	50	(AC007063) putative nucleotide-sugar transporter [Arabidopsis thaliana]
2175	LIB3602-023-Q6-K1-F4	2996012	BLASTX	627	3.00E-65	68	(AF054455) cytosolic phosphoglucose isomerase;

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2176	LIB3602-090-Q6-K6-B1	7259294	BLASTX	254	2.00E-21	42	PgiC [<i>Leavenworthia crassa</i>] (AB030200) expression of this gene product inhibits the growth of <i>E. coli</i> [<i>Mus musculus</i>]
2177	LIB3602-084-Q6-K1-B5	6755114	BLASTX	331	1.00E-30	48	peroxisomal membrane protein 20 >gi 6166491 gb AAF04855.1 AF197951_1 (AF197951) thioredoxin peroxidase PMP20 [<i>Mus musculus</i>]
2178	LIB3602-063-Q1-K6-C8	3183373	BLASTX	225	3.00E-18	48	HYPOTHETICAL 28.3 KD PROTEIN C17A5.05C IN CHROMOSOME I >gi 7490843 pir T37820 hypothetical protein SPAC17A5.05c - fission yeast (<i>Schizosaccharomyces pombe</i>) >gi 2370477 emb CAB11505.1 (Z98849) hypothetical protein [<i>Schizosaccharomyces pombe</i>] (AL162295) ribosomal protein S13-like [<i>Arabidopsis thaliana</i>]
2179	LIB3602-109-Q1-K1-H6	7329687	BLASTX	496	4.00E-55	83	(AC018848) putative aspartate aminotransferase [<i>Arabidopsis thaliana</i>]
2180	LIB3602-011-Q6-K1-G7	6751711	BLASTX	383	1.00E-36	50	(AC018848) unknown protein [<i>Arabidopsis thaliana</i>]
2181	LIB3602-012-Q6-K1-E8	6751712	BLASTX	287	2.00E-25	47	(AC018848) unknown protein [<i>Arabidopsis thaliana</i>]
2182	LIB3602-011-Q6-K1-B5	2706555	BLASTX	593	2.00E-61	67	(Y15942) succinate dehydrogenase iron-sulfur subunit [<i>Agaricus bisporus</i>]
2183	LIB3602-010-Q6-K1-E8	7302498	BLASTX	304	8.00E-28	62	(AE003796) FK506 gene product [<i>Drosophila melanogaster</i>]
2184	LIB3602-039-Q6-K1-C6	7546515	BLASTX	474	2.00E-47	72	Chain A, translation Initiation Factor Eif1a
2185	LIB3602-048-Q6-K1QA-E3	6573706	BLASTX	465	2.00E-46	56	(AC009978) T23E18.6 [<i>Arabidopsis thaliana</i>]
2186	LIB3602-115-Q1-K1-H10	6573708	BLASTX	234	2.00E-19	66	(AC009978) T23E18.8 [<i>Arabidopsis thaliana</i>]
2187	LIB3602-113-Q1-K1-E6	6735373	BLASTX	447	3.00E-54	58	(AL137082) putative protein [<i>Arabidopsis thaliana</i>]
2188	LIB3602-057-Q6-K1-G7	6323420	BLASTX	197	5.00E-15	76	Ribosomal protein S29A (S36A) (YS29); Rps29ap >gi 730461 sp P41057 R29A_YEAST 40S RIBOSOMAL PROTEIN S29-A (S36) (YS29) >gi 626904 pir S48503 ribosomal protein S29.e.A, cytosolic - yeast (<i>Saccharomyces cerevisiae</i>) >gi 287628 dbj BAA03507.1 (D14676) ribos
2189	LIB3602-051-Q6-K1-D8	7385055	BLASTX	193	2.00E-14	42	(AF216387) beta-adaptin-like protein C [<i>Arabidopsis thaliana</i>]
2190	LIB3602-116-Q1-K1-E4	7304097	BLASTX	355	2.00E-33	54	(AE003838) CG8711 gene product [<i>Drosophila melanogaster</i>]
2191	LIB3602-027-Q6-K1-F1	3687243	BLASTX	219	1.00E-17	82	(AC005169) 40S ribosomal protein S30 [<i>Arabidopsis thaliana</i>]
2192	LIB3602-078-Q6-K6-B10	7446384	BLASTX	327	4.00E-30	41	probable protein kinase - tomato >gi 237777 gb AF04722.1 (Y13273) putative protein kinase [<i>Lycopersicon esculentum</i>] >gi 5669642 gb AA04406.1 AF096250_1 (AF096250) ethylene-responsive protein kinase TCTR1 [<i>Lycopersicon esculentum</i>]
2193	LIB3602-117-Q1-K1-G11	7487986	BLASTX	281	6.00E-35	49	outer envelope membrane protein homolog T6H20.230 - <i>Arabidopsis thaliana</i> >gi 5541685 emb CAB51191.1 (AL096859) chloroplast import-associated channel homolog [<i>Arabidopsis thaliana</i>] (AF067082) mannitol dehydrogenase [<i>Apium graveolens</i>]
2194	LIB3602-009-Q6-K1-D5	3283368	BLASTX	317	6.00E-29	56	(AL138658) dynamin-like protein 4 (ADL4) [<i>Arabidopsis thaliana</i>]
2195	LIB3602-058-Q6-K1-B1	7076772	BLASTX	283	4.00E-25	47	(AE003532) Probeta2 gene product [<i>Drosophila melanogaster</i>]
2196	LIB3602-093-Q6-K6-H8	7294336	BLASTX	429	4.00E-42	58	(AL132975) glycoprotein-like [<i>Arabidopsis</i>
2197	LIB3602-073-Q1-K1-C2	7076779	BLASTX	529	8.00E-54	55	

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2198	LIB3602-116-Q1-K1-D11	2129893	BLASTX	191	1.00E-21	87	thaliana]
2199	LIB3602-011-Q6-K1-D4	7445481	BLASTX	336	3.00E-31	54	preprotein translocase secA precursor - garden pea hypothetical protein F17M5.230 - Arabidopsis thaliana >gi 4490314 emb CAB38805.1 (AL035678) putative protein [Arabidopsis thaliana] >gi 7270295 emb CAB80064.1 (AL161583) putative protein [Arabidopsis thaliana]
2200	LIB3602-045-Q6-K1-H1	5730023	BLASTX	629	1.00E-65	95	RuvB (E coli homolog)-like 2 >gi 4587311 dbj BAA76708.1 (AB024301) RuvB-like DNA helicase TIP49b [Homo sapiens] >gi 5020422 gb AAD38073.1 AF155138_1 (AF155138) RUVBL2 protein [Homo sapiens] >gi 5326998 emb CAB46270.1 (Y18417) erythrocyte cytosolic prote
2201	LIB3602-059-Q6-K1-H3	5080810	BLASTX	457	2.00E-45	46	(AC007258) Very similar to helicases [Arabidopsis thaliana]
2202	LIB3602-092-Q6-K6-B8	6449503	BLASTN	35	5.00E-10	92	Genomic Sequence For Arabidopsis thaliana Clone F15F15, Chromosome V, complete sequence
2203	LIB3602-040-Q6-K1-D3	2760327	BLASTX	481	3.00E-48	72	(AC002130) FIN21.12 [Arabidopsis thaliana]
2204	LIB3602-042-Q6-K1-A11	1708463	BLASTX	205	8.00E-16	31	IAA-AMINO ACID HYDROLASE >gi 887785 gb AAB60293.1 (U23794) ILR1 [Arabidopsis thaliana]
2205	LIB3602-026-Q6-K1-G3	586059	BLASTX	697	2.00E-73	74	LYSYL-TRNA SYNTHETASE (LYSINE--TRNA LIGASE) (LYSRS) >gi 543180 pir S43187 lysine--tRNA ligase (EC 6.1.1.6) - long-tailed hamster >gi 469122 emb CAA83505.1 (Z31711) Lysyl tRNA Synthetase [Cricetus longicaudatus]
2206	LIB3602-068-Q1-K1-A7	3980394	BLASTX	177	2.00E-12	41	(AC004561) putative zinc transporter [Arabidopsis thaliana]
2207	LIB3602-032-Q6-K1-C1	6553927	BLASTX	190	2.00E-14	86	(AC012329) putative alpha NAC [Arabidopsis thaliana] >gi 6561948 emb CAB62452.1 (AL132964) alpha NAC-like protein [Arabidopsis thaliana]
2208	LIB3602-087-Q6-K1-G11	7329665	BLASTX	329	9.00E-34	43	(AL162351) putative protein [Arabidopsis thaliana]
2209	LIB3602-054-Q6-K1-H12	4557765	BLASTX	475	1.00E-47	59	5-methyltetrahydrofolate-homocysteine methyltransferase >gi 2160699 gb AAB58906.1 (U75743) methionine synthase [Homo sapiens]
2210	LIB3602-091-Q6-K6-B9	4826686	BLASTX	388	3.00E-37	57	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1 >gi 6919862 sp Q92499 DDX1_HUMAN DEAD BOX PROTEIN 1 (DEAD BOX PROTEIN-RETINOBLASTOMA) (DBP-RB) >gi 3123574 emb CAA49992.1 (X70649) member of DEAD box protein family [Homo sapiens]
2211	LIB3602-116-Q1-K1-A3	4506701	BLASTX	235	2.00E-26	89	ribosomal protein S23 >gi 730647 sp P39028 RS23_HUMAN 40S RIBOSOMAL PROTEIN S23 >gi 543449 pir S41955 ribosomal protein S23, cytosolic - rat >gi 631360 pir S42105 ribosomal protein S23, cytosolic - human >gi 414349 dbj BAA03400.1 (D14530) ribosomal pro
2212	LIB3602-072-Q1-K1-E8	6322576	BLASTX	186	1.00E-13	32	Yjr116wp >gi 1352917 sp P47153 YJ86_YEAST HYPOTHETICAL 32.0 KD PROTEIN IN NNFI-STE24 INTERGENIC REGION >gi 1078275 pir S57139 probable membrane protein YJR116w - yeast (Saccharomyces cerevisiae) >gi 1015835 emb CAA89646.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2213	LIB3602-056-Q6-K1-G11	6566272	BLASTX	607	4.00E-63	79	(Z49616) ORF YJR116w [Saccharom (AB008016) similar to ribosomal protein S2 [Arabidopsis thaliana]
2214	LIB3602-087-Q6-K1-H2	4874265	BLASTX	595	2.00E-61	67	(AC007354) EST gb F13926 comes from this gene. [Arabidopsis thaliana]
2215	LIB3602-059-Q6-K1-E6	2982297	BLASTX	584	3.00E-60	68	(AF051233) KIAA0107-like protein [Picea mariana]
2216	LIB3602-054-Q6-K1-E11	7435895	BLASTX	145	6.00E-09	51	multicatalytic endopeptidase complex (EC 3.4.99.46) beta chain - Arabidopsis thaliana >gi 2511594 emb CAA74028.1 (Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi 2827525 emb CAA16533.1 (AL02163
2217	LIB3602-100-Q1-K1-G11	322577	BLASTX	294	3.00E-26	49	Raf protein kinase homolog CTR1 - Arabidopsis thaliana
2218	LIB3602-040-Q6-K1-C4	7573420	BLASTX	414	1.00E-40	66	(AL163816) translation releasing factor RF-1-like protein [Arabidopsis thaliana]
2219	LIB3602-055-Q6-K1-F7	2462761	BLASTX	434	9.00E-43	56	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]
2220	LIB3602-094-Q6-K6-E1	7294700	BLASTX	150	3.00E-09	59	(AE003544) CG7351 gene product [Drosophila melanogaster]
2221	LIB3602-092-Q6-K6-F10	5281319	BLASTX	197	8.00E-15	34	(AF134814) ceruloplasmin [Ovis aries]
2222	LIB3602-088-Q6-K6-F1	4587520	BLASTX	159	2.00E-10	45	(AC007060) Strong similarity to gb X71057 protein kinase from Nicotiana tabacum and contains PF 00069 eukaryotic protein kinase domain. [Arabidopsis thaliana]
2223	LIB3602-002-P1-K6-D10	3928758	BLASTX	520	1.00E-52	62	(AB007987) Lipoic acid synthase [Arabidopsis thaliana] >gi 4454462 gb AAD20909.1 (AC006234) lipoic acid synthase (LIP1) [Arabidopsis thaliana]
2224	LIB3602-049-Q6-K1-C11	2501356	BLASTX	406	1.00E-39	59	TRANSKETOLASE, CHLOROPLAST PRECURSOR (TK) >gi 1658322 emb CAA90427.1 (Z50099) transketolase precursor [Solanum tuberosum]
2225	LIB3602-104-Q1-K1-H1	2494112	BLASTX	667	6.00E-70	66	(AC002376) Match to Arabidopsis ATHKCP (gb L40948). ESTs gb ATTS0764, gb R90646, gb AA389809, gb ATTS2615 come from this gene. [Arabidopsis thaliana] >gi 3126868 gb AAC15999.1 (AF061570) potassium channel beta subunit homolog [Arabidopsis thaliana]
2226	LIB3602-038-Q6-K1-B12	6503290	BLASTX	479	5.00E-48	56	(AC011713) Similar to gb U21855 CCR4-associated factor 1 (CAF1) from Mus musculus. ESTs gb AAA394972, gb AA585812 and gb H77015 come from this gene. [Arabidopsis thaliana]
2227	LIB3602-111-Q1-K1-H3	2760362	BLASTX	190	4.00E-14	37	(AF016511) 15.9 kDa subunit of RNA polymerase II [Arabidopsis thaliana]
2228	LIB3602-004-Q1-K1-F12	3122387	BLASTX	816	2.00E-87	67	WD-40 REPEAT PROTEIN MSI1 >gi 2394229 gb AAB70242.1 (AF016846) WD-40 repeat protein [Arabidopsis thaliana]
2229	LIB3602-032-Q6-K1-B8	7076763	BLASTX	615	6.00E-64	72	(AL138658) citrate synthase-like protein [Arabidopsis thaliana]
2230	LIB3602-058-Q6-K1-B2	5566579	BLASTN	35	8.00E-10	92	Lepilemur dorsalis genomic fragment, RAPD with primer operon OPH4, clone A8b
2231	LIB3602-001-P1-K6-D3	4666287	BLASTX	251	2.00E-21	50	(D85764) cytosolic monodehydroascorbate

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2232	LIB3602-056-Q6-K1-C11	3980378	BLASTX	147	3.00E-09	46	reductase [Oryza sativa] (AC004561) putative RNA-binding protein [Arabidopsis thaliana]
2233	LIB3602-037-Q6-K1-H12	3687239	BLASTX	491	2.00E-49	66	(AC005169) putative clathrin assembly protein [Arabidopsis thaliana]
2234	LIB3602-040-Q6-K1-A6	5002553	BLASTX	239	6.00E-20	42	(AF074603) NonF [Streptomyces griseus subsp. griseus]
2235	LIB3602-025-Q6-K1-D4	6403492	BLASTX	373	1.00E-35	43	(AC010871) unknown protein [Arabidopsis thaliana]
2236	LIB3602-012-Q6-K1-D8	994736	BLASTX	145	3.00E-09	74	(M18327) LacOPZ-alpha peptide from pUC9; putative [unidentified cloning vector] >gi 994738 gb AAA75563.1 (M18328) LacOPZ-alpha peptide from pUC9; putative [Cloning vector pBGS9+] >gi 994740 gb AAA75565.1 (M18329) LacOPZ-alpha peptide from pUC9; putative (AF114386) putative protease HhoA precursor [Arabidopsis thaliana]
2237	LIB3602-006-Q1-K1-D11	6690272	BLASTX	216	5.00E-17	50	(AF114386) putative protease HhoA precursor [Arabidopsis thaliana]
2238	LIB3602-023-Q6-K1-A2	4507277	BLASTX	289	9.00E-26	38	serine/threonine kinase 2 >gi 1709347 sp P51957 STK2_HUMAN SERINE/THREONINE-PROTEIN KINASE NRK2 (SERINE/THREONINE KINASE 2) >gi 7427997 pir I78885 serine/threonine-specific protein kinase (EC 2.7.1.-) STK2 - human >gi 348245 gb AAA36658.1 (L20321) prote
2239	LIB3602-052-Q6-K1-D6	7471680	BLASTX	153	7.00E-10	37	conserved hypothetical protein - Deinococcus radiodurans (strain R1) >gi 6458157 gb AAF10050.1 AE001906_6 (AE001906) conserved hypothetical protein [Deinococcus radiodurans]
2240	LIB3602-019-Q6-K1-H3	3201626	BLASTX	143	5.00E-09	37	(AC004669) putative protein kinase [Arabidopsis thaliana]
2241	LIB3602-022-Q6-K1-G3	6970044	BLASTX	481	3.00E-48	61	(AF195243) apospory-associated protein C; APOC [Chlamydomonas reinhardtii]
2242	LIB3602-066-Q1-K6-F9	7208213	BLASTX	147	4.00E-09	41	(AF160800) constitutive photomorphogenic 11 [Oryza sativa subsp. indica]
2243	LIB3602-045-Q6-K1-B1	7241508	BLASTN	43	4.00E-15	88	Sequence 36 from Patent EP0892047
2244	LIB3602-103-Q1-K1-E6	2462752	BLASTX	345	9.00E-41	56	(AC002292) Phosphatidylinositol 3-kinase [Arabidopsis thaliana]
2245	LIB3602-085-Q6-K1-D8	2493046	BLASTX	193	2.00E-14	55	ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR >gi 82297 pir A41740 H+-transporting ATP synthase (EC 3.6.1.34) delta' chain precursor - sweet potato >gi 217938 dbj BAA01511.1 (D10660) mitochondrial F1-ATPase delta subunit [Ipomoea batatas]
2246	LIB3602-079-Q6-K6-C5	7303555	BLASTX	338	2.00E-31	48	(AE003824) CG8983 gene product [Drosophila melanogaster]
2247	LIB3602-013-Q6-K1-G3	484466	BLASTX	345	3.00E-32	41	glucan endo-1,3-beta-D-glucosidase (EC 3.2.1.39) precursor - Bacillus circulans (strain IAM1165) >gi 452882 gb AAC60453.1 (S67033) beta-1,3-glucanase {EC 3.2.1.39} [Bacillus circulans, IAM1165, Peptide, 877 aa] >gi 601878 dbj BAA04469.1 (D17519) beta-1,
2248	LIB3602-017-Q6-K1-A8	7362989	BLASTN	34	2.00E-09	82	Homo sapiens partial mRNA, clone c4-1b12
2249	LIB3602-035-Q1-K1-A7	2500295	BLASTX	275	6.00E-24	50	50S RIBOSOMAL PROTEIN L21 >gi 7428682 pir S75901 ribosomal protein L21 - Synechocystis sp. (strain PCC 6803)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2250	LIB3602-049-Q6-K1-A4	2501188	BLASTX	194	3.00E-15	71	>gi 1653446 dbj BAA18360.1 (D90913) 50S ribosomal protein L21 [Synechocystis sp.] THIAZOLE BIOSYNTHETIC ENZYME PRECURSOR (ARA6) >gi 2129750 pir S71191 thiamin biosynthesis protein thi4 - Arabidopsis thaliana >gi 1113783 gb AAC97124.1 (U17589) Thi1 protein [Arabidopsis thaliana]
2251	LIB3602-018-Q6-K1-D11	400989	BLASTX	150	9.00E-10	56	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24) >gi 322771 pir A45113 ribosomal protein L24 precursor - common tobacco >gi 170273 gb AAA34086.1 (M87838) ribosomal protein L24 [Nicotiana tabacum] >gi 170324 gb AAA34114.1 (M87839) ribosomal prote
2252	LIB3602-086-Q6-K1-E1	6598752	BLASTX	300	6.00E-27	64	(AC007290) putative chromosome associated protein [Arabidopsis thaliana]
2253	LIB3602-059-Q6-K1-E8	7434997	BLASTX	268	3.00E-23	32	lysosomal acid lipase - human >gi 505053 gb AAB60328.1 (U08464) lysosomal acid lipase [Homo sapiens] >gi 506431 emb CAA83495.1 (Z31690) lysosomal acid lipase [Homo sapiens]
2254	LIB3602-026-Q6-K1-H10	7462772	BLASTX	170	9.00E-12	30	hypothetical protein TM0484 - Thermotoga maritima (strain MSB8) >gi 4980995 gb AAD35569.1 AE001726_3 (AE001726) pyrimidine precursor biosynthesis enzyme, putative [Thermotoga maritima] (AC002294) Unknown protein [Arabidopsis thaliana]
2255	LIB3602-042-Q6-K1-B1	2443886	BLASTX	363	2.00E-34	64	(AC002294) Unknown protein [Arabidopsis thaliana]
2256	LIB3602-028-Q6-K1-D7	133891	BLASTX	222	7.00E-18	50	40S RIBOSOMAL PROTEIN S26 (DS31) >gi 71054 pir R3FF26 ribosomal protein S26 - fruit fly (Drosophila melanogaster) >gi 8494 emb CAA32463.1 (X14247) ribosomal protein S31 [Drosophila melanogaster] >gi 4469169 emb CAB38441.1 (X13625) ribosomal protein S31
2257	LIB3602-119-Q1-K1-B6	2500243	BLASTX	151	3.00E-10	72	50S RIBOSOMAL PROTEIN L6 >gi 2127652 pir S62827 ribosomal protein L6 - Mycoplasma pneumoniae (strain ATCC 29342) >gi 2146617 pir S73977 ribosomal protein L6 - Mycoplasma pneumoniae (SGC3) (ATCC 29342) >gi 1215708 gb AAC43701.1 (U34795) RplF [Mycoplasma
2258	LIB3602-074-Q1-K1-D5	476608	BLASTN	37	4.00E-11	91	Drosophila melanogaster ribosomal protein L19 mRNA
2259	LIB3602-032-Q6-K1-C3	7572912	BLASTX	150	2.00E-09	38	(AL163763) putative protein [Arabidopsis thaliana]
2260	LIB3602-048-Q6-K1QA-E2	1707018	BLASTX	287	2.00E-25	52	(U78721) putative related to microbial divalent cation tolerance proteins [Arabidopsis thaliana]
2261	LIB3602-059-Q6-K1-A2	6630731	BLASTX	425	1.00E-41	45	(AL132958) RNA helicase-like protein [Arabidopsis thaliana]
2262	LIB3602-074-Q1-K1-A9	1703457	BLASTX	288	2.00E-25	51	CATION-TRANSPORTING ATPASE CA1 >gi 1103646 emb CAA63790.1 (X93592) CA1 [Dunaliella bioculata]
2263	LIB3602-085-Q6-K1-E4	6630733	BLASTX	510	1.00E-64	71	(AL132958) Cytochrom P450-like protein [Arabidopsis thaliana]
2264	LIB3602-119-Q1-K1-H10	1350947	BLASTX	156	1.00E-11	78	40S RIBOSOMAL PROTEIN S18 >gi 1076216 pir S51145 ribosomal protein S18.e,

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							cytosolic - Chlamydomonas reinhardtii >gi 624957 emb CAA58668.1 (X83693) ribosomal protein S18 [Chlamydomonas reinhardtii] >gi 1587084 prf 2205351A ribosomal protein S18 [Chlamyd
2265	LIB3602-103-Q1-K1-E1	7209723	BLASTX	244	2.00E-20	43	(AB034912) WD-repeat like sequence [Homo sapiens]
2266	LIB3602-014-Q6-K1-A2	2511590	BLASTX	301	2.00E-27	58	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] >gi 3421111 gb AAC32070.1 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]
2267	LIB3602-007-Q1-K1-H12	7488326	BLASTX	315	1.00E-28	56	SEN1 protein homolog T20K24.14 - Arabidopsis thaliana >gi 3176714 gb AAD12029.1 (AC002392) putative DNA2-NAM7 helicase family protein [Arabidopsis thaliana]
2268	LIB3602-039-Q6-K1-D5	7485815	BLASTX	279	1.00E-24	60	hypothetical protein F19I3.9 - Arabidopsis thaliana >gi 3033382 gb AAC12826.1 (AC004238) unknown protein [Arabidopsis thaliana]
2269	LIB3602-035-Q1-K1-E5	7297653	BLASTX	232	4.00E-19	40	(AE003628) CG4968 gene product [Drosophila melanogaster]
2270	LIB3602-118-Q1-K1-H9	7484927	BLASTX	146	6.00E-09	57	DNA-3-methyladenine glycosidase I homolog F18B3.160 - Arabidopsis thaliana >gi 4835239 emb CAB42917.1 (AL049862) putative DNA-3-methyladenine glycosidase [Arabidopsis thaliana]
2271	LIB3602-039-Q6-K1-B2	5669636	BLASTX	328	3.00E-30	44	(AF096247) ethylene-responsive elongation factor EF-Ts precursor [Lycopersicon esculentum]
2272	LIB3602-077-Q6-K6-G10	5669638	BLASTX	417	1.00E-40	74	(AF096248) ethylene-responsive RNA helicase [Lycopersicon esculentum]
2273	LIB3602-039-Q6-K1-E12	7459497	BLASTX	194	1.00E-14	32	hypothetical protein sl0886 - Synechocystis sp. (strain PCC 6803) >gi 1001204 dbj BAA10444.1 (D64003) hypothetical protein [Synechocystis sp.]
2274	LIB3602-012-Q6-K1-C11	404015	BLASTX	174	9.00E-24	59	(U02032) ribosomal protein L23a [Homo sapiens]
2275	LIB3602-094-Q6-K6-F8	1172599	BLASTX	354	3.00E-33	54	PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C5) (TAS-F22/FAFP98) >gi 600387 emb CAA47753.1 (X67338) proteasome subunit [Arabidopsis thaliana]
2276	LIB3602-084-Q6-K1-H1	1942873	BLASTX	210	2.00E-16	47	Thioredoxin H (Oxidized Form), Nmr, 23 Structures
2277	LIB3602-061-Q6-K1-E4	7512679	BLASTX	484	1.00E-48	68	hypothetical protein DKFZp434N241.1 - human (fragment) >gi 5911980 emb CAB55960.1 (AL117492) hypothetical protein [Homo sapiens]
2278	LIB3602-040-Q6-K1-E7	7488346	BLASTX	316	6.00E-29	62	spliceosome-associated protein SAP62 homolog T26B15.16 - Arabidopsis thaliana >gi 3298548 gb AAC25942.1 (AC004681) putative spliceosome-associated protein [Arabidopsis thaliana]
2279	LIB3602-077-Q6-K6-H12	7484782	BLASTX	286	3.00E-25	42	4-alpha-glucanotransferase homolog T20B5.4 - Arabidopsis thaliana >gi 2623298 gb AAB86444.1 (AC002409) 4-alpha-glucanotransferase [Arabidopsis thaliana]
2280	LIB3602-034-Q6-K1-E4	732535	BLASTN	39	5.00E-13	90	Volvox carteri oxygen-evolving enhancer protein 3 mRNA, complete cds
2281	LIB3602-108-Q1-K1-D1	7484784	BLASTX	219	1.00E-17	33	ABC-type transport protein homolog F12C20.5 - Arabidopsis thaliana >gi 3426037 gb AAC32236.1 (AC005168) putative ABC transporter [Arabidopsis

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2282	LIB3602-111-Q1-K1-B8	3043694	BLASTX	182	3.00E-23	38	thaliana] (AB011157) KIAA0585 protein [Homo sapiens]
2283	LIB3602-109-Q1-K1-D4	2492772	BLASTX	178	9.00E-23	73	ALCOHOL DEHYDROGENASE CLASS III (GLUTATHIONE-DEPENDENT FORMALDEHYDE DEHYDROGENASE) (FDH) (FALDH) (GSH-FDH) >gi 1498024 gb AAB06322.1 (U63931) glutathione-dependent formaldehyde dehydrogenase [Arabidopsis thaliana]
2284	LIB3602-039-Q6-K1-F2	7431747	BLASTX	176	2.00E-12	52	probable acyl-CoA dehydrogenase - Mycobacterium tuberculosis (strain H37RV) >gi 2911026 emb CAA17519.1 (AL021958) fadE9 [Mycobacterium tuberculosis]
2285	LIB3602-085-Q6-K1-F10	7485823	BLASTX	162	9.00E-11	45	hypothetical protein F1C12.70 - Arabidopsis thaliana >gi 2982432 emb CAA18240.1 (AL022224) putative protein [Arabidopsis thaliana] >gi 7268810 emb CAB79015.1 (AL161552) putative protein [Arabidopsis thaliana]
2286	LIB3602-041-Q6-K1-A10	7459661	BLASTX	242	4.00E-20	42	transcription initiation factor IIA gamma chain homolog T22A6.270 - Arabidopsis thaliana >gi 2826882 emb CAA11524.1 (AJ223634) transcription factor IIA small subunit [Arabidopsis thaliana] >gi 5051786 emb CAB45079.1 (AL078637) transcription factor IIA s (AF139466) chlorophyll a/b binding protein CP29 [Vigna radiata]
2287	LIB3602-020-Q6-K1-F8	4689382	BLASTX	315	7.00E-29	57	(AF013216) isocitrate lyase [Myxococcus xanthus]
2288	LIB3602-048-Q6-K1QA-C6	2811131	BLASTX	181	5.00E-13	66	(AC007591) Strong similarity to gb AF096285 serine-threonine kinase receptor-associated protein from Mus musculus and contains 5 PF 00400 WD40, G-beta repeat domains. EST gb F14050 comes from this gene. [Arabidopsis thaliana]
2289	LIB3602-111-Q1-K1-D11	5103845	BLASTX	279	2.00E-32	49	hypothetical protein T20K18.240 - Arabidopsis thaliana >gi 4586265 emb CAB41006.1 (AL049640) putative protein [Arabidopsis thaliana] >gi 7267991 emb CAB78331.1 (AL161535) putative protein [Arabidopsis thaliana]
2290	LIB3602-086-Q6-K1-B5	7487272	BLASTX	171	8.00E-12	32	(AC005311) hypothetical protein [Arabidopsis thaliana]
2291	LIB3602-001-P1-K6-C3	3746062	BLASTX	150	2.00E-09	45	hypothetical protein T29H11.100 - Arabidopsis thaliana >gi 4678350 emb CAB41160.1 (AL049659) putative protein [Arabidopsis thaliana]
2292	LIB3602-084-Q6-K1-H3	7452056	BLASTX	160	1.00E-10	67	(AF198092) RP42 [Mus musculus]
2293	LIB3602-088-Q6-K6-H4	6166507	BLASTX	168	8.00E-12	56	(AL162875) 3-oxoacyl-[acyl-carrier-protein] synthase-like protein [Arabidopsis thaliana]
2294	LIB3602-036-Q6-K1-D3	7406456	BLASTX	256	9.00E-22	38	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H) >gi 82412 pir S05012 photosystem I protein psaH precursor - barley >gi 19093 emb CAA34218.1 (X16092) 10.2 kDa photosystem I polypeptide [Hordeum vulga]
2295	LIB3602-092-Q6-K6-C8	131196	BLASTX	499	3.00E-50	69	L-ascorbate peroxidase (EC 1.11.1.11), cytosolic - cucumber >gi 1669585 dbj BAA13671.1 (D88649) cytosolic ascorbate peroxidase [Cucumis sativus]
2296	LIB3602-032-Q6-K1-A7	7484752	BLASTX	355	2.00E-33	54	(AC013354) F15H18.4 [Arabidopsis thaliana]
2297	LIB3602-019-Q6-K1-G8	6714305	BLASTX	183	2.00E-13	38	(AL162754) putative
2298	LIB3602-053-Q6-K1-H10	7379607	BLASTX	381	2.00E-36	59	

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2299	LIB3602-078-Q6-K6-C4	267073	BLASTX	669	4.00E-72	93	amidophosphoribosyltransferase [Neisseria meningitidis] TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin beta chain - Arabidopsis thaliana >gi 166898 gb AAA32881.1 (M84700) beta-2 tubulin [Arabidopsis thaliana] >gi 166900 gb AAA32882.1 (M84701) beta-3 tubulin [Arabidopsis thaliana]
2300	LIB3602-003-Q1-K1-F11	4885539	BLASTX	234	3.00E-19	51	protein-L-isoaspartate (D-aspartate) O-methyltransferase >gi 1332399 dbj BAA05028.1 (D25545) PIMT isozyme I [Homo sapiens] >gi 1332403 dbj BAA05030.1 (D25547) PIMT isozyme I [Homo sapiens]
2301	LIB3602-078-Q6-K6-G4	4929769	BLASTX	170	9.00E-12	68	(AF151908) CGI-150 protein [Homo sapiens]
2302	LIB3602-021-Q6-K1-A2	1710560	BLASTX	166	9.00E-12	93	60S RIBOSOMAL PROTEIN L40 (CEP52)
2303	LIB3602-006-Q1-K1-D6	5107214	BLASTX	196	1.00E-14	63	(AF150113) small zinc finger-like protein [Oryza sativa]
2304	LIB3602-009-Q6-K1-D6	549986	BLASTX	228	1.00E-18	46	(U13149) possible apospory-associated protein [Pennisetum ciliare]
2305	LIB3602-101-Q1-K1-E8	7486379	BLASTX	376	5.00E-36	57	hypothetical protein F3L17.100 - Arabidopsis thaliana >gi 5262764 emb CAB45912.1 (AL080283) putative protein [Arabidopsis thaliana] >gi 7270056 emb CAB79871.1 (AL161579) putative protein [Arabidopsis thaliana] (Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
2306	LIB3602-118-Q1-K1-E11	3617770	BLASTX	358	1.00E-33	56	(Y14329) threonyl-tRNA synthetase [Arabidopsis thaliana]
2307	LIB3602-111-Q1-K1-G9	1351669	BLASTX	206	5.00E-16	36	HYPOTHETICAL 44.3 KD PROTEIN C1F7.07C IN CHROMOSOME I >gi 2130298 pir S62579 hypothetical protein SPAC1F7.07c - fission yeast (Schizosaccharomyces pombe) >gi 7492832 pir T38101 probable plasma membrane iron permease - fission yeast (Schizosaccharomyces
2308	LIB3602-046-Q6-K1-E8	1350778	BLASTX	547	5.00E-56	66	60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) >gi 2119118 pir I50151 acidic ribosomal phosphoprotein - chicken >gi 453474 gb AAC38020.1 (L28704) acidic ribosomal phosphoprotein [Gallus gallus] (AF002248) PSI light-harvesting antenna chlorophyll a/b-binding protein [Pisum sativum]
2309	LIB3602-048-Q6-K1QA-G3	6470348	BLASTX	305	1.00E-27	52	(AF073697) cysteine synthase [Oryza sativa]
2310	LIB3602-092-Q6-K6-A11	4574139	BLASTX	545	8.00E-57	58	(AF073697) cysteine synthase [Oryza sativa]
2311	LIB3602-015-Q6-K1-B8	7431577	BLASTX	537	9.00E-55	62	probable pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) E1 beta chain - Synechocystis sp. (strain PCC 6803) >gi 1652524 dbj BAA17445.1 (D90906) pyruvate dehydrogenase E1 beta subunit [Synechocystis sp.]
2312	LIB3602-041-Q6-K1-C8	7469613	BLASTX	264	1.00E-22	61	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1001629 dbj BAA10360.1 (D64002) hypothetical protein [Synechocystis sp.]
2313	LIB3602-092-Q6-K6-E2	2493650	BLASTX	268	4.00E-23	79	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi 1167858 emb CAA93139.1 (Z68903) chaperonin [Secale cereale]
2314	LIB3602-055-Q6-K1-H11	21309	BLASTX	150	8.00E-10	45	(X57955) 28kD RNA binding protein [Spinacia oleracea]
2315	LIB3602-005-Q1-K1-D7	5103820	BLASTX	359	8.00E-34	34	(AC007591) Similar to gb Z70524 PDR5-like ABC

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							transporter from Spirodela polyrrhiza and is a member of the PF00005 ABC transporter family. ESTs gb N97039 and gb T43169 come from this gene. [Arabidopsis thaliana]
2316	LIB3602-115-Q1-K1-B2	586845	BLASTX	235	3.00E-19	42	PROBABLE MALTOSE O-ACETYLTRANSFERASE (MALTOSE TRANSACETYLASE) >gi 2126884 pir I39920 probable O-acetyltransferase (EC 2.3.1.-) yyaI - Bacillus subtilis >gi 438465 gb AAA64343.1 (L16865) Probable operon with orfF. Possible alternative initiation codon, b
2317	LIB3602-037-Q6-K1-E3	1350930	BLASTX	513	6.00E-52	84	40S RIBOSOMAL PROTEIN S13
2318	LIB3602-060-Q6-K1-F6	4914332	BLASTX	164	4.00E-11	57	(AC005489) F14N23.18 [Arabidopsis thaliana]
2319	LIB3602-030-Q6-K1-G8	6093612	BLASTX	563	6.00E-58	71	PYRUVATE DEHYDROGENASE E1 COMPONENT BETA SUBUNIT, MITOCHONDRIAL PRECURSOR (PDHE1-B) >gi 520478 gb AAA52225.1 (U09137) pyruvate dehydrogenase E1 beta subunit [Arabidopsis thaliana] >gi 1090498 prf 2019230A pyruvate dehydrogenase [Arabidopsis thaliana]
2320	LIB3602-074-Q1-K1-F6	5911363	BLASTX	210	2.00E-16	50	(AF159699) putative host factor [Nicotiana tabacum]
2321	LIB3602-103-Q1-K1-H10	7469637	BLASTX	145	1.00E-16	62	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1001676 dbj BAA10411.1 (D64002) hypothetical protein [Synechocystis sp.]
2322	LIB3602-102-Q1-K1-H8	3327210	BLASTX	161	1.00E-10	30	(AB014598) KIAA0698 protein [Homo sapiens]
2323	LIB3602-107-Q1-K1-H2	7544040	BLASTX	696	2.00E-73	67	(AL163641) acetyl/propionyl CoA carboxylase, beta subunit [Streptomyces coelicolor A3(2)]
2324	LIB3602-088-Q6-K6-E12	7428213	BLASTX	233	5.00E-19	45	endopeptidase Clp ATP-binding chain C - Synechococcus sp. (strain PCC 7942) >gi 755163 gb AAB67745.1 (U16134) ClpC [Synechococcus sp.]
2325	LIB3602-026-Q6-K1-H11	81679	BLASTX	199	4.00E-15	61	acyl carrier protein precursor (clone 34C02) - rape
2326	LIB3602-048-Q6-K1QA-B11	6730727	BLASTX	492	1.00E-49	60	(AC018849) putative acetylornithine transaminase [Arabidopsis thaliana]
2327	LIB3602-055-Q6-K1-H9	3913791	BLASTX	269	2.00E-23	48	GLUTAMATE--CYSTEINE LIGASE PRECURSOR (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS) >gi 7489004 pir T04332 glutamate--cysteine ligase (EC 6.3.2.2) - tomato >gi 2407615 gb AAB71230.1 (AF017983) gamma-glutamylcysteine synthetase [Lycopersicon escul
2328	LIB3602-005-Q1-K1-H11	266567	BLASTX	329	3.00E-30	48	MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi 421956 pir S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi 21493 emb CAA46990.1 (X66284)
2329	LIB3602-063-Q1-K6-G10	6984214	BLASTX	481	2.00E-68	62	(AF228639) lipoamide dehydrogenase precursor [Arabidopsis thaliana]
2330	LIB3602-087-Q6-K1-F7	7499051	BLASTX	328	4.00E-47	62	hypothetical protein F13H8.7 - Caenorhabditis elegans >gi 722377 gb AAC46683.1 (U23139) highly similar to beta-ureidopropionase (SP:BUP_RAT) [Caenorhabditis elegans]
2331	LIB3602-028-Q6-K1-H12	7488521	BLASTX	163	6.00E-11	43	cysteine proteinase inhibitor BCPI-2 - turnip >gi 1256424 gb AAA96316.1 (U51119) cysteine

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2332	LIB3602-076-Q6-K6-C3	6984216	BLASTX	238	6.00E-29	52	proteinase inhibitor [Brassica rapa] (AF228640) lipoamide dehydrogenase precursor [Arabidopsis thaliana]
2333	LIB3602-076-Q6-K6-H12	4884860	BLASTX	157	8.00E-11	60	(AF133118) nucleic acid binding protein [Oryza sativa]
2334	LIB3602-050-Q6-K1-E12	7488367	BLASTX	203	1.00E-15	37	thiamin pyrophosphokinase homolog F16B22.24 - Arabidopsis thaliana >gi 3341695 gb AAC27477.1 (AC003672) putative thiamin pyrophosphokinase [Arabidopsis thaliana]
2335	LIB3602-101-Q1-K1-A3	7106101	BLASTX	358	2.00E-42	67	(AL157917) ap-1 golgi-associated clathrin assembly protein complex component [Schizosaccharomyces pombe]
2336	LIB3602-111-Q1-K1-E7	1749716	BLASTX	359	6.00E-34	63	(D89254) similar to Saccharomyces cerevisiae dihydroxy-acid dehydratase precursor, SWISS-PROT Accession Number P39522 [Schizosaccharomyces pombe]
2337	LIB3602-073-Q1-K1-G6	2398531	BLASTX	263	1.00E-22	70	(Y13726) Transcription factor [Arabidopsis thaliana]
2338	LIB3602-088-Q6-K6-A3	7077174	BLASTX	163	2.00E-11	60	(AB035256) eukaryotic polypeptide chain release factor 3 [Oryctolagus cuniculus]
2339	LIB3602-050-Q6-K1-H2	7290447	BLASTX	166	2.00E-11	49	(AE003429) CG2934 gene product [Drosophila melanogaster]
2340	LIB3602-109-Q1-K1-E11	7442647	BLASTX	212	6.00E-22	37	hypothetical protein F14M4.17 - Arabidopsis thaliana >gi 3522943 gb AAC34225.1 (AC004411) putative ABC transporter [Arabidopsis thaliana]
2341	LIB3602-067-Q1-K1-A9	115385	BLASTX	243	3.00E-20	48	CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR (LHCI TYPE III CAB-4) (LHCP) >gi 166646 gb AAA32760.1 (M63931) light-harvesting chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 6522530 emb CAB61973.1 (AL132955) CHLOROPHYLL A-B BINDING PROTEIN 4 PR
2342	LIB3602-011-Q6-K1-G9	7488383	BLASTX	202	2.00E-15	40	transcription factor IID 30K chain homolog F28M20.90 - Arabidopsis thaliana >gi 2072626 emb CAA73389.1 (Y12904) hypothetical protein [Arabidopsis thaliana] >gi 3281856 emb CAA19751.1 (AL031004) Transcription factor II homolog [Arabidopsis thaliana] >gi
2343	LIB3602-023-Q6-K1-F8	7489278	BLASTX	254	1.00E-21	36	thioredoxin-like protein CDSP32, chloroplast - potato >gi 2582822 emb CAA71103.1 (Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]
2344	LIB3602-107-Q1-K1-G9	2129726	BLASTX	467	2.00E-46	51	DNA-directed RNA polymerase (EC 2.7.7.6) II 35.5K chain A - Arabidopsis thaliana >gi 514318 gb AAB03741.1 (L34770) RNA polymerase II third largest subunit [Arabidopsis thaliana] >gi 4544370 gb AAD22281.1 AC006920_5 (AC006920) DNA-directed RNA polymerase
2345	LIB3602-017-Q6-K1-A1	7488371	BLASTX	329	1.00E-30	66	thioredoxin reductase homolog T32G6.20 - Arabidopsis thaliana >gi 2618704 gb AAB84351.1 (AC002510) putative thioredoxin reductase [Arabidopsis thaliana]
2346	LIB3602-080-Q6-K6-A6	4887543	BLASTX	195	1.00E-14	75	(AJ012278) ATP-dependent Clp protease subunit ClpP [Arabidopsis thaliana] >gi 5360579 dbj BAA82065.1 (AB022326) nClpP1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2347	LIB3602-045-Q6-K1-F6	7469824	BLASTX	195	1.00E-14	32	[Arabidopsis thaliana] hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1653953 dbj BAA18863.1 (D90917)
2348	LIB3602-030-Q6-K1-E1	7485867	BLASTX	211	1.00E-16	37	hypothetical protein [Synechocystis sp.] hypothetical protein F20D22.10 - Arabidopsis thaliana >gi 3142297 gb AAC16748.1 (AC002411) Contains similarity to serine/threonine protein phosphatase gb X83099 from S. cerevisiae.
2349	LIB3602-085-Q6-K1-C8	7302133	BLASTX	251	3.00E-21	35	[Arabidopsis thaliana] (AE003781) CG1416 gene product [Drosophila melanogaster]
2350	LIB3602-055-Q6-K1-D12	2351580	BLASTX	317	5.00E-29	60	(U82433) thymidine diphospho-glucose 4-6-dehydratase homolog [Prunus armeniaca]
2351	LIB3602-077-Q6-K6-C11	7462403	BLASTX	464	4.00E-46	56	heat shock protein HslV - Thermotoga maritima (strain MSB8) >gi 4981034 gb AAD35606.1 AE001728_7 (AE001728) heat shock protein HslV [Thermotoga maritima]
2352	LIB3602-040-Q6-K1-A9	2494744	BLASTX	400	8.00E-39	85	GLUTAMINE SYNTHETASE CYTOSOLIC ISOZYME (GLUTAMATE--AMMONIA LIGASE) (GS1) >gi 7437922 pir T08088 glutamate--ammonia ligase (EC 6.3.1.2), cytosolic - Chlamydomonas reinhardtii >gi 1353876 gb AAB01817.1 (U46207) glutamine synthetase [Chlamydomonas reinhard
2353	LIB3602-012-Q6-K1-B3	122805	BLASTX	180	7.00E-13	32	6-HYDROXY-D-NICOTINE OXIDASE (6-HDNO) >gi 580720 emb CAA29416.1 (X05999) 6-hydroxy-D-nicotine oxidase [Arthrobacter oxidans]
2354	LIB3602-049-Q6-K1-B9	99772	BLASTX	209	2.00E-16	68	ubiquitin / ribosomal protein S27a.2 - Arabidopsis thaliana >gi 166936 gb AAA32907.1 (J05540) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi 3522953 gb AAC34235.1 (AC004411) ubiquitin extension protein (UBQ6) [Arabidopsis thaliana]
2355	LIB3602-103-Q1-K1-F9	6679160	BLASTX	216	3.00E-17	39	nucleoredoxin >gi 1854550 emb CAA63408.1 (X92750) red-1 [Mus musculus]
2356	LIB3602-023-Q6-K1-D9	7594543	BLASTX	300	6.00E-27	41	(AL163972) putative protein [Arabidopsis thaliana]
2357	LIB3602-087-Q6-K1-F10	7489244	BLASTX	275	1.00E-32	57	hypothetical protein R1 - potato >gi 3287270 emb CAA70725.1 (Y09533) involved in starch metabolism [Solanum tuberosum]
2358	LIB3602-118-Q1-K1-H4	7019967	BLASTX	156	3.00E-10	53	(AK000099) unnamed protein product [Homo sapiens]
2359	LIB3602-115-Q1-K1-B7	1729938	BLASTX	185	2.00E-13	45	THIOREDOXIN-LIKE PROTEIN SLR0233 >gi 7430831 pir S76386 thioredoxin M-1 - Synechocystis sp. (strain PCC 6803) >gi 1001610 dbj BAA10238.1 (D64000) thioredoxin M [Synechocystis sp.]
2360	LIB3602-093-Q6-K6-A4	7225945	BLASTX	175	2.00E-12	41	(AE002426) queuine tRNA-ribosyltransferase [Neisseria meningitidis]
2361	LIB3602-023-Q6-K1-F12	595780	BLASTX	159	2.00E-10	43	(U13871) lacZ alpha peptide [unidentified cloning vector]
2362	LIB3602-008-Q6-K1-E11	7023065	BLASTX	606	7.00E-63	66	(AK001667) unnamed protein product [Homo sapiens]
2363	LIB3602-111-Q1-K1-B3	6651403	BLASTX	159	1.00E-16	29	(AF180734) dynamin-like protein 5 [Arabidopsis thaliana]
2364	LIB3602-018-Q6-K1-G8	6562305	BLASTX	259	3.00E-22	42	(AL133421) putative protein [Arabidopsis thaliana]
2365	LIB3602-014-Q6-K1-F7	6562306	BLASTX	219	1.00E-17	45	(AL133421) diacylglycerol kinase (ATDGK1)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2366	LIB3602-016-Q6-K1-C10	1729930	BLASTX	204	8.00E-16	43	[Arabidopsis thaliana] THREONINE DEHYDRATASE BIOSYNTHETIC (THREONINE DEAMINASE) >gi 1113117 gb AAA83215.1 (U40630) L- threonine deaminase [Burkholderia cepacia]
2367	LIB3602-115-Q1-K1-H4	7432656	BLASTX	158	3.00E-10	40	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) - fission yeast (Schizosaccharomyces pombe) >gi 2414635 emb CAB16382.1 (Z99260) putative nadh-dehydrogenase [Schizosaccharomyces pombe]
2368	LIB3602-012-Q6-K1-F5	7489245	BLASTX	241	2.00E-20	50	kinesin heavy chain-like protein (clone PKCBP) - potato >gi 1369852 gb AAB37756.1 (L46702) kinesin heavy chain-like protein [Solanum tuberosum]
2369	LIB3602-034-Q6-K1-B9	7428204	BLASTX	353	4.00E-33	51	carboxypeptidase D (EC 3.4.16.6) precursor - barley >gi 1731990 emb CAA70815.1 (Y09602) serine carboxypeptidase II, CP-MII [Hordeum vulgare]
2370	LIB3602-007-Q1-K1-A11	2498140	BLASTX	181	6.00E-13	41	APAG PROTEIN (CORD PROTEIN) >gi 1003021 gb AAA79339.1 (U24176) CorD [Salmonella typhimurium]
2371	LIB3602-076-Q6-K6-F10	7433551	BLASTX	749	1.00E-79	71	glycine hydroxymethyltransferase (EC 2.1.2.1) F20D10.50 - Arabidopsis thaliana >gi 4467099 emb CAB37533.1 (AL035538) glycine hydroxymethyltransferase like protein [Arabidopsis thaliana] >gi 6899945 emb CAB71289.1 (AJ271726) serine hydroxymethyl transfer
2372	LIB3602-001-P1-K6-F1	4006886	BLASTX	284	4.00E-25	53	(Z99708) putative protein [Arabidopsis thaliana] >gi 7270635 emb CAB80352.1 (AL161590) putative protein [Arabidopsis thaliana]
2373	LIB3602-041-Q6-K1-E7	6562319	BLASTX	173	5.00E-12	35	(AL133421) putative protein [Arabidopsis thaliana]
2374	LIB3602-064-Q1-K6-B10	1350977	BLASTX	144	2.00E-12	71	PROBABLE 40S RIBOSOMAL PROTEIN S30
2375	LIB3602-002-P1-K6-F7	2924772	BLASTX	203	1.00E-15	48	(AC002334) unknown protein [Arabidopsis thaliana]
2376	LIB3602-011-Q6-K1-C5	2506275	BLASTX	199	3.00E-19	52	CHAPERONIN CPN60-1, MITOCHONDRIAL PRECURSOR (HSP60-1)
2377	LIB3602-084-Q6-K1-G5	6692692	BLASTX	310	4.00E-28	54	(AC007592) F12K11.10 [Arabidopsis thaliana]
2378	LIB3602-047-Q6-K1-E3	5523979	BLASTX	252	2.00E-21	54	(AF104025) polyprotein [Bovine viral diarrhea virus-2]
2379	LIB3602-077-Q6-K6-D2	7485688	BLASTX	283	3.00E-25	60	hypothetical protein F18A5.110 - Arabidopsis thaliana >gi 4455301 emb CAB36836.1 (AL035528) putative protein [Arabidopsis thaliana] >gi 7268076 emb CAB78414.1 (AL161537) putative protein [Arabidopsis thaliana]
2380	LIB3602-100-Q1-K1-E6	7298579	BLASTX	431	3.00E-51	56	(AE003662) CG9987 gene product [Drosophila melanogaster]
2381	LIB3602-095-Q6-K6-E4	3327204	BLASTX	465	3.00E-46	52	(AB014595) KIAA0695 protein [Homo sapiens]
2382	LIB3602-095-Q6-K6-D5	3327206	BLASTX	199	4.00E-15	37	(AB014596) KIAA0696 protein [Homo sapiens]
2383	LIB3602-036-Q6-K1-E10	7300338	BLASTX	181	5.00E-13	41	(AE003721) CG7217 gene product [Drosophila melanogaster]
2384	LIB3602-066-Q1-K6-E11	7488307	BLASTX	162	8.00E-11	47	ribosomal protein L14 homolog T24A18.40 - Arabidopsis thaliana >gi 4490705 emb CAB38839.1 (AL035680) ribosomal protein L14-like protein [Arabidopsis thaliana] >gi 7269562 emb CAB79564.1 (AL161566) ribosomal protein L14-like protein [Arabidopsis thaliana]

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2385	LIB3602-040-Q6-K1-E12	5757449	BLASTX	157	2.00E-10	73	(AB021315) L41 ribosomal protein [Coprinus cinereus]
2386	LIB3602-013-Q6-K1-D9	7437876	BLASTX	285	1.00E-25	64	probable acid--CoA ligase (EC 6.2.1.-) fadD35 - Mycobacterium tuberculosis (strain H37RV) >gi 2113938 emb CAB08923.1 (Z95556) fadD35 [Mycobacterium tuberculosis]
2387	LIB3602-042-Q6-K1-D5	2499954	BLASTX	331	1.00E-30	54	URACIL PHOSPHORIBOSYLTRANSFERASE (UMP PYROPHOSPHORYLASE) (UPRTASE) >gi 7427938 pir S74616 uracil phosphoribosyltransferase (EC 2.4.2.9) upp - Synechocystis sp. (strain PCC 6803) >gi 1651841 dbj BAA16768.1 (D90900) uracil phosphoribosyltransferase [Synec
2388	LIB3602-012-Q6-K1-F7	81235	BLASTX	731	2.00E-77	76	chlorophyll a/b-binding protein - Chlamydomonas reinhardtii
2389	LIB3602-055-Q6-K1-C1	5902062	BLASTX	364	1.00E-34	62	polymerase (RNA) III (DNA directed) (155kD) >gi 3122765 sp O14802 RPC1_HUMAN DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (RPC155) >gi 2460208 gb AAB86536.1 (AF021351) RNA polymerase III largest subunit [Homo sapiens]
2390	LIB3602-091-Q6-K6-H1	5454054	BLASTX	162	9.00E-11	35	splicing factor, arginine/serine-rich 7 (35kD) >gi 3929380 sp Q16629 SFR7_HUMAN SPLICING FACTOR, ARGININE/SERINE-RICH 7 (SPLICING FACTOR 9G8) >gi 2136194 pir A57198 splicing factor, arginine/serine-rich 7 - human >gi 506402 gb AAA35495.1 (L22253) 9G8 sp
2391	LIB3602-065-Q1-K6-G12	3982576	BLASTX	803	7.00E-86	76	(AF023140) imidazoleglycerol phosphate dehydratase [Thlaspi goesingense]
2392	LIB3602-083-Q6-K6-G7	6226702	BLASTX	555	8.00E-57	62	40S RIBOSOMAL PROTEIN S8 >gi 7440237 pir B06330.1 (U64436) ribosomal protein S8 [Zea mays]
2393	LIB3602-003-Q1-K1-E4	2464901	BLASTX	232	4.00E-19	41	(Z99708) putative protein [Arabidopsis thaliana] >gi 7270628 emb CAB80345.1 (AL161590) putative protein [Arabidopsis thaliana]
2394	LIB3602-009-Q6-K1-C9	3372671	BLASTX	162	5.00E-11	54	(AF061286) gamma-adaptin 1 [Arabidopsis thaliana] >gi 4704741 gb AAD28247.1 AF124524_1 gamma-adaptin 1 [Arabidopsis thaliana]
2395	LIB3602-041-Q6-K1-C1	7512095	BLASTX	175	3.00E-12	33	scavenger receptor cysteine-rich protein precursor - sea urchin (Strongylocentrotus purpuratus) >gi 4165053 gb AAD08654.1 (AF064259) scavenger receptor cysteine-rich protein type 12 precursor [Strongylocentrotus purpuratus]
2396	LIB3602-074-Q1-K1-B5	6225655	BLASTX	328	3.00E-30	51	MALATE SYNTHASE >gi 2811132 gb AAB97829.1 (AF013216) Mls [Myxococcus xanthus]
2397	LIB3602-078-Q6-K6-B4	7297250	BLASTX	292	6.00E-26	61	(AE003617) CG5261 gene product [alt 2] [Drosophila melanogaster]
2398	LIB3602-101-Q1-K1-D3	7436983	BLASTX	404	3.00E-50	79	probable imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19) - wheat (fragment) >gi 551331 gb AAA93197.1 (U02690) imidazoleglycerolphosphate dehydratase [Triticum aestivum]

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2399	LIB3602-001-P1-K6-G7	6056371	BLASTX	653	3.00E-68	77	(AC009894) nucleolar protein [Arabidopsis thaliana]
2400	LIB3602-051-Q6-K1-B1	2116650	BLASTX	757	9.00E-84	94	(AB004044) alpha-1-antitrypsin [Cercopithecus aethiops]
2401	LIB3602-092-Q6-K6-C2	6900314	BLASTX	238	1.00E-19	81	(AJ250663) putative proteinase inhibitor [Hordeum vulgare]
2402	LIB3602-062-Q6-K1-F10	113324	BLASTX	271	1.00E-23	57	ACYLPHOSPHATASE, MUSCLE TYPE ISOZYME (ACYLPHOSPHATE PHOSPHOHYDROLASE) (ISOZYME TU1) >gi 67797 pir QPTK acylphosphatase (EC 3.6.1.7) Tu1, skeletal muscle - turkey >gi 223821 prf 1001154A acylphosphatase [Meleagris gallopavo]
2403	LIB3602-115-Q1-K1-D12	3293555	BLASTX	712	3.00E-75	70	(AF072931) chlorophyll a/b binding protein [Medicago sativa]
2404	LIB3602-062-Q6-K1-D4	7225376	BLASTX	177	7.00E-13	64	(AE002373) 50S ribosomal protein L18 [Neisseria meningitidis] >gi 7378885 emb CAB83428.1 (AL162752) 50S ribosomal protein L18 [Neisseria meningitidis]
2405	LIB3602-016-Q6-K1-E8	1707981	BLASTX	259	3.00E-22	59	GLUTAREDOXIN >gi 1076561 pir S54825 glutaredoxin - castor bean
2406	LIB3602-014-Q6-K1-B10	6754812	BLASTX	179	9.00E-13	51	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 2 (8 kDa) >gi 4836511 gb AAD30475.1 AF124786_1 (AF124786) NADH-ubiquinone oxidoreductase B8 subunit [Mus musculus]
2407	LIB3602-095-Q6-K6-B5	1408302	BLASTX	348	1.00E-43	43	(U61987) phosphoprotein phosphatase A [Dictyostelium discoideum]
2408	LIB3602-061-Q6-K1-H3	7510484	BLASTX	151	1.00E-09	44	hypothetical protein Y75B8A.26 - Caenorhabditis elegans >gi 3980042 emb CAA22110.1 (AL033514) similar to ABC transporters ; ABC transporter transmembrane region. [Caenorhabditis elegans]
2409	LIB3602-025-Q6-K1-G6	5381319	BLASTX	658	5.00E-69	79	(AF091621) ubiquitin-conjugating enzyme E2 [Catharanthus roseus]
2410	LIB3602-069-Q1-K1-A6	2565436	BLASTX	562	1.00E-57	58	(AF028842) DegP protease precursor [Arabidopsis thaliana]
2411	LIB3602-094-Q6-K6-C8	4587571	BLASTX	277	2.00E-24	50	(AC006550) Belongs to the PF01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]
2412	LIB3602-045-Q6-K1-C7	7484375	BLASTX	310	3.00E-28	49	envelope protein LIP-36G2, low CO2 inducible - Chlamydomonas reinhardtii >gi 2459575 gb AAB71744.1 (U75346) envelope protein [Chlamydomonas reinhardtii]
2413	LIB3602-061-Q6-K1-G7	4775576	BLASTX	591	4.00E-61	67	(AJ238785) MUS1 protein [Zea mays]
2414	LIB3602-076-Q6-K6-B6	2499966	BLASTX	162	1.00E-10	50	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A) >gi 7443146 pir T16962 photosystem I chain PSI-E - wood tobacco >gi 632722 gb AAB31704.1 (S72356) photosystem I subunit PSI-E [Nicotiana glauca, leaves, Peptide Chloroplast, 141 aa]
2415	LIB3602-002-P1-K6-B7	3025293	BLASTX	259	3.00E-22	83	RAS-RELATED PROTEIN YPTC6 >gi 1363476 pir JC4108 GTP-binding protein yptC6 - Chlamydomonas reinhardtii >gi 806728 gb AAA82729.1 (U13169) YptC6 [Chlamydomonas reinhardtii]
2416	LIB3602-115-Q1-K1-G6	6652886	BLASTX	255	7.00E-22	80	(AF123394) 26S proteasome AAA-ATPase subunit

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							RPT5a [Arabidopsis thaliana] >gi 7596759 gb AAF64530.1 (AC009606) 26S proteasome AAA-ATPase subunit RPT5a [Arabidopsis thaliana]
2417	LIB3602-052-Q6-K1-F6	7489990	BLASTX	441	1.00E-43	63	40s ribosomal protein s4-2 - fission yeast (Schizosaccharomyces pombe) >gi 6018736 emb CAB57920.1 (AL121794) 40s ribosomal protein s4-2 [Schizosaccharomyces pombe]
2418	LIB3602-076-Q6-K6-F7	3121830	BLASTX	725	9.00E-77	67	CHROMATIN ASSEMBLY FACTOR 1 P55 SUBUNIT (CAF-1 P55 SUBUNIT) (DCAF-1) (NUCLEOSOME REMODELING FACTOR 55 KD SUBUNIT) (NURF-55) >gi 1407828 gb AAB37257.1 (U62388) chromatin assembly factor 1 p55 subunit [Drosophila melanogaster] >gi 7299974 gb AAF55146.1 (A(Y17225) cyclin-dependent protein kinase p34cdc2 [Lycopersicon esculentum]
2419	LIB3602-052-Q6-K1-C5	3123614	BLASTX	678	2.00E-71	79	PHOSPHATIDATE CYTIDYLYLTRANSFERASE (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE) >gi 2181182 emb CAA63969.1 (X94306) CDP-diacylglycerol syn (AC000348) T7N9.4 [Arabidopsis thaliana]
2421	LIB3602-027-Q6-K1-H1	2213584	BLASTX	192	2.00E-14	50	(AL132966) diaminopimelate epimerase-like protein [Arabidopsis thaliana]
2422	LIB3602-112-Q1-K1-F9	6729509	BLASTX	345	3.00E-32	68	(L40632) ankyrin 3 [Mus musculus]
2423	LIB3602-067-Q1-K1-D8	710550	BLASTX	214	8.00E-17	39	(L40632) ankyrin 3 [Mus musculus]
2424	LIB3602-010-Q6-K1-H2	710551	BLASTX	246	1.00E-20	37	(AF123391) 26S proteasome AAA-ATPase subunit RPT2a [Arabidopsis thaliana]
2425	LIB3602-047-Q6-K1-H2	6652880	BLASTX	704	2.00E-74	93	(AC006532) unknown protein [Arabidopsis thaliana]
2426	LIB3602-027-Q6-K1-G10	4406787	BLASTX	160	1.00E-10	59	(AB005903) AtPH1 [Arabidopsis thaliana]
2427	LIB3602-059-Q6-K1-H1	5926716	BLASTX	412	4.00E-40	57	phytoene synthase (EC 2.5.1.-) - green alga (Dunaliella bardawil) >gi 1916990 gb AAB51287.1 (U91900) phytoene synthase [Dunaliella bardawil]
2428	LIB3602-077-Q6-K6-C6	7484346	BLASTX	728	4.00E-77	68	(AP000836) Similar to ISP42-like protein (AF051231) [Oryza sativa]
2429	LIB3602-027-Q6-K1-A3	6539563	BLASTX	325	6.00E-30	47	(D87750) farnesyl cysteine carboxyl methyltransferase [Xenopus laevis]
2430	LIB3602-003-Q1-K1-F3	1906804	BLASTX	254	9.00E-22	46	proteasome (prosome, macropain) subunit, alpha type 4 >gi 5757663 gb AAD50538.1 AF060093_1 (AF060093) proteasome subunit C9 [Mus musculus]
2431	LIB3602-057-Q6-K1-F5	6755196	BLASTX	151	3.00E-19	66	(AC007443) putative chlorophyll a/b binding protein [Arabidopsis thaliana]
2432	LIB3602-003-Q1-K1-D2	4874296	BLASTX	146	3.00E-11	51	(AC005662) hypothetical protein [Arabidopsis thaliana]
2433	LIB3602-019-Q6-K1-D6	3894197	BLASTX	249	5.00E-21	68	glutamate N-acetyltransferase (EC 2.3.1.35) - Synechocystis sp. (strain PCC 6803) >gi 1653293 dbj BAA18208.1 (D90912) ornithine acetyltransferase [Synechocystis sp.]
2434	LIB3602-030-Q6-K1-D4	7448559	BLASTX	312	2.00E-28	63	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]
2435	LIB3602-013-Q6-K1-C11	2688839	BLASTX	144	8.00E-09	60	

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2436	LIB3602-062-Q6-K1-H7	7630021	BLASTX	289	1.00E-25	35	(AL132960) pasticcino 1 [Arabidopsis thaliana]
2437	LIB3602-070-Q1-K1-D7	1173223	BLASTX	152	6.00E-13	64	40S RIBOSOMAL PROTEIN S11 >gi 454848 gb AAC14469.1 (L28831) ribosomal protein S11 [Glycine max]
2438	LIB3602-055-Q6-K1-D6	4506589	BLASTX	267	3.00E-23	39	RNA 3'-terminal phosphate cyclase >gi 2500648 sp O00442 RTC1_HUMAN RNA 3'-TERMINAL PHOSPHATE CYCLASE 1 (RNA-3'-PHOSPHATE CYCLASE 1) (RNA CYCLASE 1) >gi 2125812 emb CAA72364.1 (Y11651) phosphate cyclase [Homo sapiens]
2439	LIB3602-076-Q6-K6-H9	7404436	BLASTX	156	4.00E-10	56	60S RIBOSOMAL PROTEIN L6 >gi 7490046 pir T41499 60s ribosomal protein l6 - fission yeast (Schizosaccharomyces pombe) >gi 3821337 emb CAA21874.1 (AL033127) 60s ribosomal protein l6 [Schizosaccharomyces pombe]
2440	LIB3602-087-Q6-K1-C3	7485401	BLASTX	145	5.00E-09	62	hypothetical protein F12C20.6 - Arabidopsis thaliana >gi 3426051 gb AAC32250.1 (AC005168) putative Na ⁺ dependent ileal bile acid transporter [Arabidopsis thaliana]
2441	LIB3602-016-Q6-K1-A4	3157934	BLASTX	523	3.00E-53	66	(AC002131) Similar to hypothetical protein F09E5.8 gb U37429 from C. elegans. ESTs gb T42019 and gb N97000 come from this gene. [Arabidopsis thaliana]
2442	LIB3602-019-Q6-K1-E9	267002	BLASTX	261	2.00E-22	50	SULFITE REDUCTASE (FERREDOXIN) >gi 66219 pir RDYCS7 sulfite reductase (ferredoxin) (EC 1.8.7.1) - Synechococcus sp >gi 38930 emb CAA77809.1 (Z11755) ferredoxin-sulfite reductase [Synechococcus PCC6301]
2443	LIB3602-026-Q6-K1-A4	7480951	BLASTX	591	4.00E-61	64	probable long-chain-fatty-acid-CoA ligase - Streptomyces coelicolor >gi 4455741 emb CAB36604.1 (AL035478) putative long-chain-fatty-acid-CoA ligase [Streptomyces coelicolor A3(2)]
2444	LIB3602-059-Q6-K1-D4	6729515	BLASTX	244	2.00E-20	44	(AL132966) protein kinase-like protein [Arabidopsis thaliana]
2445	LIB3602-067-Q1-K1-C4	4836870	BLASTX	408	1.00E-39	56	(AC007260) 50S Ribosomal protein L13 [Arabidopsis thaliana] >gi 7572938 emb CAA60775.1 (X87333) ribosomal protein L13 [Arabidopsis thaliana]
2446	LIB3602-043-Q6-K1-F8	7447850	BLASTX	351	4.00E-33	80	hypothetical protein F3L17.50 - Arabidopsis thaliana >gi 5262759 emb CAB45907.1 (AL080283) putative protein [Arabidopsis thaliana] >gi 7270051 emb CAB79866.1 (AL161579) putative protein [Arabidopsis thaliana]
2447	LIB3602-042-Q6-K1-H3	7413562	BLASTX	230	9.00E-19	53	(AL162973) 60S ribosomal protein-like [Arabidopsis thaliana]
2448	LIB3602-048-Q6-K1QA-G9	7630237	BLASTX	352	4.00E-33	44	(AP001859) ESTs AU082761(S5084),D42006(S5084) correspond to a region of the predicted gene.~Similar to Caenorhabditis elegans chromosome 3, cosmid C17G10; alcohol dehydrogenase/ribitol dehydrogenase. (U28739) [Oryza sativa]
2449	LIB3602-061-Q6-K1-E5	3122785	BLASTX	591	4.00E-61	86	40S RIBOSOMAL PROTEIN S14 >gi 7440341 pir T07974 ribosomal protein S14 - yellow lupine >gi 2565340 gb AAB81972.1 (AF026079) ribosomal protein S14 [Lupinus luteus]
2450	LIB3602-047-Q6-K1-A6	6524184	BLASTX	318	4.00E-29	49	(AC011914) putative mutT protein [Arabidopsis

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2451	LIB3602-011-Q6-K1-G8	5262856	BLASTX	281	9.00E-25	60	thaliana] (AJ238095) Lsm3 protein [Homo sapiens] >gi 5919147 gb AAD56227.1 AF182289_1 (AF182289) U6 snRNA-associated Sm-like protein Lsm3 [Homo sapiens]
2452	LIB3602-034-Q6-K1-B7	5757653	BLASTX	149	2.00E-09	43	(AF060088) proteasome subunit C2 [Mus musculus]
2453	LIB3602-066-Q1-K6-F12	5007086	BLASTX	449	2.00E-44	59	(AF155334) NADP-specific isocitrate dehydrogenase [Oryza sativa]
2454	LIB3602-026-Q6-K1-G2	730536	BLASTX	179	2.00E-13	84	60S RIBOSOMAL PROTEIN L23 >gi 7440849 pir T03693 ribosomal protein L17 - common tobacco >gi 310933 gb AAA34113.1 (L18915) 60S ribosomal protein subunit L17 [Nicotiana tabacum]
2455	LIB3602-059-Q6-K1-B4	7492749	BLASTX	281	9.00E-25	45	probable nadh-cytochrome b5 reductase - fission yeast (Schizosaccharomyces pombe) >gi 3560228 emb CAA20696.1 (AL031530) putative nadh-cytochrome b5 reductase [Schizosaccharomyces pombe]
2456	LIB3602-040-Q6-K1-F10	416583	BLASTX	241	4.00E-20	75	ACETYL-COENZYME A SYNTHETASE (ACETATE--COA LIGASE) (ACYL-ACTIVATING ENZYME) >gi 7437823 pir D65215 acetate--CoA ligase (EC 6.2.1.1) - Escherichia coli >gi 396404 gb AAC43163.1 (U00006) acetyl-CoA synthetase [Escherichia coli] >gi 1790505 gb AAC77039.1 (Z33611) phosphoglycerate mutase [Zea mays]
2457	LIB3602-092-Q6-K6-A2	551288	BLASTX	710	5.00E-75	88	(AF085148) 3-oxoacyl-[acyl-carrier-protein] synthase [Capsicum chinense]
2458	LIB3602-066-Q1-K6-B11	3599489	BLASTX	162	9.00E-11	40	(AF059510) 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit [Arabidopsis thaliana] >gi 7021224 gb AAF35259.1 AF059511_1 (AF059511) 3-methylcrotonyl-CoA carboxylase nonbiotinylated subunit [Arabidopsis thaliana]
2459	LIB3602-085-Q6-K1-H3	7021222	BLASTX	219	5.00E-25	56	ACYL CARRIER PROTEIN, MITOCHONDRIAL PRECURSOR (ACP) (NADH-UBIQUINONE OXIDOREDUCTASE 9.6 KD SUBUNIT) (MTACP-1) >gi 7442278 pir T01589 probable acyl carrier protein F16B22.11 - Arabidopsis thaliana >gi 903689 gb AAB96840.1 (L23574) acyl carrier protein pr
2461	LIB3602-027-Q6-K1-E4	7469427	BLASTX	177	1.00E-12	33	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1001449 dbj BAA10074.1 (D63999) hypothetical protein [Synechocystis sp.]
2462	LIB3602-011-Q6-K1-A7	7431396	BLASTX	242	3.00E-20	61	xanthine dehydrogenase homolog T1111.140 - Arabidopsis thaliana >gi 5123707 emb CAB45451.1 (AL079347) xanthine dehydrogenase [Arabidopsis thaliana] >gi 7270441 emb CAB80207.1 (AL161586) xanthine dehydrogenase [Arabidopsis thaliana] (AL162875) putative protein [Arabidopsis thaliana]
2463	LIB3602-002-P1-K6-G12	7406448	BLASTX	147	6.00E-09	40	(U82756) WD splicing factor Hprp4p [Homo sapiens]
2464	LIB3602-042-Q6-K1-A7	2853277	BLASTX	152	7.00E-10	60	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1653680 dbj BAA18592.1 (D90915) pyruvate dehydrogenase E1 component, alpha
2465	LIB3602-070-Q1-K1-G3	7431559	BLASTX	502	1.00E-50	73	

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2466	LIB3602-025-Q6-K1-E2	132076	BLASTX	523	4.00E-53	67	subunit [Synechocystis sp.] RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR (RUBISCO SMALL SUBUNIT 1) >gi 68109 pir RKKMS1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain 1 precursor - Chlamydomonas reinhardtii
2467	LIB3602-046-Q6-K1-B9	7486523	BLASTX	231	3.00E-19	45	hypothetical protein F6H11.40 - Arabidopsis thaliana >gi 2827702 emb CAA16675.1 (AL021684) predicted protein [Arabidopsis thaliana]
2468	LIB3602-109-Q1-K1-F4	7298362	BLASTX	152	1.00E-09	51	(AE003653) ApepP gene product [Drosophila melanogaster]
2469	LIB3602-030-Q6-K1-H3	6066383	BLASTX	414	2.00E-40	51	(AJ011926) Mg-protoporphyrin IX [Hordeum vulgare]
2470	LIB3602-112-Q1-K1-B4	1905979	BLASTX	219	2.00E-17	46	(U81052) oligosaccharyltransferase subunit homolog [Mus musculus]
2471	LIB3602-041-Q6-K1-H6	167433	BLASTN	34	3.00E-09	89	C.reinhardtii ribulose 1,5-bisphosphate carboxylase/oxygenase activase mRNA, complete cds
2472	LIB3602-025-Q6-K1-A2	7485629	BLASTX	365	1.00E-34	57	hypothetical protein F17K2.15 - Arabidopsis thaliana >gi 2979552 gb AAC06161.1 (AC003680) unknown protein [Arabidopsis thaliana]
2473	LIB3602-015-Q6-K1-G7	129699	BLASTX	582	5.00E-60	71	PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN) >gi 99946 pir S14414 proliferating cell nuclear antigen - soybean (fragment) >gi 18726 emb CAA39239.1 (X55706) proliferating cell nuclear antigen [Glycine max]
2474	LIB3602-046-Q6-K1-B4	3122952	BLASTX	144	8.00E-09	32	TIPD PROTEIN >gi 7489899 pir T08602 protein TipD - slime mold (Dictyostelium discoideum) >gi 2407788 gb AAB70659.1 (AF019236) TipD [Dictyostelium discoideum]
2475	LIB3602-025-Q6-K1-B7	2773404	BLASTX	324	8.00E-30	46	(AF041255) pyridoxal kinase [Sus scrofa]
2476	LIB3602-118-Q1-K1-D4	7380038	BLASTX	167	7.00E-21	60	(AL162755) putative GTP-binding protein [Neisseria meningitidis]
2477	LIB3602-010-Q6-K1-A3	7487074	BLASTX	556	5.00E-57	61	hypothetical protein T16H5.240 - Arabidopsis thaliana (fragment) >gi 3250697 emb CAA19705.1 (AL024486) putative protein [Arabidopsis thaliana] >gi 7268784 emb CAB78990.1 (AL161551) putative protein [Arabidopsis thaliana]
2478	LIB3602-062-Q6-K1-F2	7021047	BLASTX	174	3.00E-12	41	(AK000759) unnamed protein product [Homo sapiens]
2479	LIB3602-108-Q1-K1-B4	7503535	BLASTX	181	4.00E-13	34	hypothetical protein F46B3.9 - Caenorhabditis elegans >gi 3877232 emb CAB04398.1 (Z81540) predicted using Genefinder [Caenorhabditis elegans]
2480	LIB3602-070-Q1-K1-C8	7630059	BLASTX	227	2.00E-18	33	(AL353013) putative protein [Arabidopsis thaliana]
2481	LIB3602-090-Q6-K6-A3	6226735	BLASTX	199	4.00E-15	37	PUTATIVE ACETYLTRANSFERASE C18B11.09C IN CHROMOSOME I >gi 7492354 pir T37905 probable acetyltransferase - fission yeast (Schizosaccharomyces pombe) >gi 4150918 emb CAA90593.1 (Z50728) putative acetyltransferase [Schizosaccharomyces pombe]
2482	LIB3602-052-Q6-K1-B8	7486331	BLASTX	175	2.00E-12	52	hypothetical protein F28M20.60 - Arabidopsis thaliana >gi 3281853 emb CAA19748.1 (AL031004) putative protein [Arabidopsis thaliana] >gi 7270078 emb CAB79893.1 (AL161579)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2483	LIB3602-086-Q6-K1-B7	6970282	BLASTX	323	1.00E-29	64	putative protein [Arabidopsis thaliana] (AC021666) unknown protein [Arabidopsis thaliana]
2484	LIB3602-016-Q6-K1-A6	1707992	BLASTX	280	1.00E-24	51	SERINE HYDROXYMETHYLTRANSFERASE (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi 485099 gb AAB53830.1 (U00048) Contains similarity to Pfam domain: PF00464 (SHMT), Score=954.1, E-value=9.9e-287, N=1 [Caenorhabditis elegans]
2485	LIB3602-114-Q1-K1-F4	226788	BLASTX	166	3.00E-11	35	erythrocyte ankyrin [Homo sapiens]
2486	LIB3602-100-Q1-K1-C4	7019397	BLASTX	150	2.00E-09	34	GDP-mannose pyrophosphorylase B >gi 5052351 gb AAD38516.1 AF135421_1 (AF135421) GDP-mannose pyrophosphorylase B [Homo sapiens]
2487	LIB3602-008-Q6-K1-G8	6056388	BLASTX	790	2.00E-84	94	(AC009324) 26S proteasome ATPase subunit [Arabidopsis thaliana]
2488	LIB3602-085-Q6-K1-H6	4263697	BLASTX	185	9.00E-14	46	(AC006223) 60S ribosomal protein L27 [Arabidopsis thaliana]
2489	LIB3602-029-Q6-K1-G2	7484385	BLASTX	267	4.00E-23	68	L-ascorbate peroxidase (EC 1.11.1.11) precursor - Chlamydomonas reinhardtii >gi 2887338 emb CAA11265.1 (AJ223325) ascorbate peroxidase [Chlamydomonas reinhardtii]
2490	LIB3602-115-Q1-K1-E2	7466728	BLASTX	173	4.00E-12	39	probable iron-sulfur-binding protein b0947 - Escherichia coli >gi 1787179 gb AAC74033.1 (AE000196) orf, hypothetical protein [Escherichia coli]
2491	LIB3602-100-Q1-K1-A4	7487059	BLASTX	180	5.00E-13	38	hypothetical protein T16B24.22 - Arabidopsis thaliana >gi 3402689 gb AAC28992.1 (AC004697) unknown protein [Arabidopsis thaliana]
2492	LIB3602-059-Q6-K1-C8	6978917	BLASTX	327	2.00E-30	60	(AC021665) putative histidinol-phosphate aminotransferase [Arabidopsis thaliana]
2493	LIB3602-040-Q6-K1-H7	6807962	BLASTX	461	4.00E-46	72	(AL137410) hypothetical protein [Homo sapiens]
2494	LIB3602-115-Q1-K1-B9	7340654	BLASTX	550	3.00E-63	68	(AL162506) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]
2495	LIB3602-029-Q6-K1-G11	7630068	BLASTX	206	6.00E-16	71	(AL353032) v-ATPase subunit D (vATPD) [Arabidopsis thaliana]
2496	LIB3602-066-Q1-K6-C5	122090	BLASTX	426	1.00E-41	98	HISTONE H3 >gi 81287 pir S00940 histone H3 - Volvox carteri >gi 2119017 pir S59581 histone H3 (clones CH-II and CH-III) - Chlamydomonas reinhardtii >gi 21985 emb CAA30035.1 (X06963) put. histone H3 [Volvox carteri] >gi 21988 emb CAA30037.1 (X06964) put. histone H3 [Volvox carteri]
2497	LIB3602-037-Q6-K1-G8	7206844	BLASTX	187	6.00E-14	50	(AC006834) contains similarity to NADH-ubiquinone oxidoreductase 18 KD subunits [Caenorhabditis elegans]
2498	LIB3602-052-Q6-K1-A7	6165265	BLASTX	341	7.00E-32	62	(AJ250733) translation elongation factor 1-alpha [Dreissena polymorpha]
2499	LIB3602-118-Q1-K1-E1	7576173	BLASTX	158	6.00E-14	33	(AL163912) putative protein [Arabidopsis thaliana]
2500	LIB3602-108-Q1-K1-D10	4689334	BLASTX	271	8.00E-29	63	(AF132555) BcDNA.GM07659 [Drosophila melanogaster]
2501	LIB3602-030-Q6-K1-D2	7630065	BLASTX	580	7.00E-60	77	(AL353032) ribosomal protein L11-like [Arabidopsis thaliana]
2502	LIB3602-053-Q6-K1-B1	6056399	BLASTX	188	8.00E-14	61	(AC009324) AP2 domain containing protein RAP2.12 [Arabidopsis thaliana]
2503	LIB3602-111-Q1-K1-C12	7485448	BLASTX	273	8.00E-24	44	hypothetical protein F13M23.170 - Arabidopsis thaliana >gi 4455246 emb CAB36745.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							(AL035523) putative protein [Arabidopsis thaliana] >gi 7269353 emb CAB79412.1 (AL161562) putative protein [Arabidopsis thaliana] (M74441) ribulose 1,5-bisphosphate carboxylase large subunit [Chlorella-like algae]
2504	LIB3602-038-Q6-K1-H11	167253	BLASTX	849	2.00E-91	94	(AF132552) BcDNA.GM01838 [Drosophila melanogaster] >gi 7301261 gb AAF56391.1 (AE003750) OstStt3 gene product [Drosophila melanogaster]
2505	LIB3602-042-Q6-K1-C2	4689328	BLASTX	408	1.00E-39	59	(AC005287) translation initiation factor [Arabidopsis thaliana]
2506	LIB3602-039-Q6-K1-G11	4585973	BLASTX	241	5.00E-20	66	(AC006951) 3-oxoacyl carrier protein synthase [Arabidopsis thaliana]
2507	LIB3602-018-Q6-K1-H1	4587598	BLASTX	246	1.00E-22	47	(X05025) ribosomal protein L14 [Xenopus laevis]
2508	LIB3602-087-Q6-K1-A10	65068	BLASTX	274	5.00E-24	50	(M79328) alpha-amylase [Solanum tuberosum]
2509	LIB3602-051-Q6-K1-G7	1220453	BLASTX	383	9.00E-37	47	(M79328) alpha-amylase [Solanum tuberosum]
2510	LIB3602-041-Q6-K1-B12	7473394	BLASTX	361	1.00E-34	65	probable acyl-CoA dehydrogenase - Deinococcus radiodurans (strain R1) >gi 6460476 gb AAF12182.1 AE001862_8 (AE001862) acyl-CoA dehydrogenase, putative [Deinococcus radiodurans]
2511	LIB3602-072-Q1-K1-B12	7437759	BLASTX	510	2.00E-51	51	arginine--tRNA ligase (EC 6.1.1.19) - Arabidopsis thaliana >gi 2632105 emb CAB11468.1 (Z98760) arginyl-tRNA synthetase [Arabidopsis thaliana] >gi 4539426 emb CAB38959.1 (AL049171) arginyl-tRNA synthetase [Arabidopsis thaliana] >gi 7269482 emb CAB79485.1
2512	LIB3602-104-Q1-K1-H8	3421104	BLASTX	450	1.00E-44	71	(AF043531) 20S proteasome beta subunit PBB2 [Arabidopsis thaliana]
2513	LIB3602-004-Q1-K1-E10	3212610	BLASTX	386	5.00E-37	57	Chain A, Sulfite Oxidase From Chicken Liver >gi 3212611 pdb 1SOX B Chain B, Sulfite Oxidase From Chicken Liver
2514	LIB3602-003-Q1-K1-G7	3041702	BLASTX	205	8.00E-16	30	TRIACYLGLYCEROL LIPASE, GASTRIC PRECURSOR (GASTRIC LIPASE) (GL) >gi 2204113 emb CAA74198.1 (Y13899) triacylglycerol lipase [Canis familiaris]
2515	LIB3602-064-Q1-K6-A9	2500381	BLASTX	270	1.00E-26	65	60S RIBOSOMAL PROTEIN L44 P (L41) (L41 P-TYPE)
2516	LIB3602-079-Q6-K6-B4	3025188	BLASTX	285	4.00E-25	52	HYPOTHETICAL 11.9 KD PROTEIN SLR1846 >gi 7448385 pir S75164 hypothetical protein slr1846 - Synechocystis sp. (strain PCC 6803) >gi 1652154 dbj BAA17078.1 (D90903) hypothetical protein [Synechocystis sp.]
2517	LIB3602-059-Q6-K1-G8	4587605	BLASTX	224	5.00E-18	41	(AC006951) putative mutT domain protein [Arabidopsis thaliana]
2518	LIB3602-089-Q6-K6-H5	21983	BLASTN	64	3.00E-27	97	Volvox carteri H3-I and H4-I genes for histones H3 and H4
2519	LIB3602-030-Q6-K1-C7	4263711	BLASTX	515	3.00E-52	63	(AC006223) putative CCR4-associated factor [Arabidopsis thaliana]
2520	LIB3602-084-Q6-K1-G12	6056404	BLASTX	409	1.00E-39	50	(AC009525) Similar to cullin proteins [Arabidopsis thaliana]
2521	LIB3602-039-Q6-K1-B9	4263714	BLASTX	540	4.00E-55	59	(AC006223) unknown protein [Arabidopsis thaliana]
2522	LIB3602-105-Q1-K1-E2	2583129	BLASTX	621	1.00E-64	64	(AC002387) putative methionine aminopeptidase [Arabidopsis thaliana]
2523	LIB3602-113-Q1-K1-B2	1931647	BLASTX	573	6.00E-59	56	(U95973) endomembrane protein EMP70 precursor isolog [Arabidopsis thaliana]
2524	LIB3602-105-Q1-K1-H5	6649217	BLASTX	199	4.00E-15	50	(AF165422) suppressor of K+ transport growth

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2525	LIB3602-101-Q1-K1-D5	7573355	BLASTX	156	3.00E-10	61	defect-like protein [Mesembryanthemum crystallinum] (AL163812) diaminopimelate decarboxylase-like protein [Arabidopsis thaliana]
2526	LIB3602-094-Q6-K6-F11	6119520	BLASTX	517	2.00E-52	50	(AC011560) unknown protein [Arabidopsis thaliana]
2527	LIB3602-017-Q6-K1-D10	1583601	BLASTX	200	2.00E-15	76	zeta carotene desaturase [Capsicum annuum]
2528	LIB3602-051-Q6-K1-C11	3122638	BLASTX	345	4.00E-49	66	PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1 >gi 1076381 pir S49820 PRL1 protein - Arabidopsis thaliana >gi 577733 emb CAA58031.1 (X82824) PRL1 [Arabidopsis thaliana] >gi 577735 emb CAA58032.1 (X82825) PRL1 [Arabidopsis thaliana] >gi 2244947 emb CA
2529	LIB3602-046-Q6-K1-G12	2501449	BLASTX	228	1.00E-18	47	UBIQUITIN-LIKE PROTEIN SMT3 >gi 7446816 pir T04102 smt3 protein - rice >gi 1668773 emb CAA67922.1 (X99608) ubiquitin-like protein [Oryza sativa]
2530	LIB3602-106-Q1-K1-C4	1323548	BLASTN	70	1.00E-30	90	Chlamydomonas reinhardtii carbonic anhydrase precursor (beta-CA1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
2531	LIB3602-103-Q1-K1-H4	6321942	BLASTX	300	5.00E-27	61	ribosomal protein (weak similarity); Imp3p >gi 418596 sp P32899 IMP3_YEAST U3 SMALL NUCLEOLAR RIBONUCLEOPROTEIN PROTEIN IMP3 >gi 485540 pir S33911 probable ribosomal protein YHR148w - yeast (Saccharomyces cerevisiae) >gi 4014 emb CAA49237.1 (X69480) uOR
2532	LIB3602-057-Q6-K1-E2	6119523	BLASTX	275	6.00E-24	32	(AC011560) putative amino acid transporter [Arabidopsis thaliana]
2533	LIB3602-052-Q6-K1-C11	7431230	BLASTX	184	1.00E-13	50	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - tomato (fragment) >gi 804817 gb AAA66051.1 (L36647) malic enzyme [Lycopersicon esculentum]
2534	LIB3602-109-Q1-K1-G7	3264759	BLASTX	444	5.00E-44	70	(AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
2535	LIB3602-068-Q1-K1-G3	7475184	BLASTX	260	3.00E-22	35	hypothetical protein ymaE - Bacillus subtilis >gi 2634109 emb CAB13609.1 (Z99113) ymaE [Bacillus subtilis]
2536	LIB3602-044-Q6-K1-H6	4506489	BLASTX	411	5.00E-40	57	replication factor C (activator 1) 3 (38kD) >gi 3915601 sp P40938 AC13_HUMAN ACTIVATOR 1 38 KD SUBUNIT (REPLICATION FACTOR C 38 KD SUBUNIT) (A1 38 KD SUBUNIT) (RF-C 38 KD SUBUNIT) (RFC38) >gi 7444557 pir T09573 replication factor C 38K chain - human >gi
2537	LIB3602-040-Q6-K1-D11	7486039	BLASTX	321	2.00E-29	40	hypothetical protein F23F1.14 - Arabidopsis thaliana >gi 3420057 gb AAC31858.1 (AC004680) putative ABC transporter [Arabidopsis thaliana]
2538	LIB3602-004-Q1-K1-F10	7446679	BLASTX	152	3.00E-15	49	peptide methionine sulfoxide reductase - Methanobacterium thermoautotrophicum (strain Delta H) >gi 2621609 gb AAB85041.1 (AE000836) peptide methionine sulfoxide reductase [Methanobacterium thermoautotrophicum]
2539	LIB3602-014-Q6-K1-D10	6716785	BLASTX	632	7.00E-66	90	(AF220539) 40s ribosomal protein S23 [Euphorbia esula]
2540	LIB3602-057-Q6-K1-D4	4826972	BLASTX	315	1.00E-28	44	RNA binding motif protein 8

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2541	LIB3602-016-Q6-K1-E6	2274859	BLASTX	318	4.00E-29	74	>gi 4455129 gb AAD21089.1 (AF127761) ribonucleoprotein RBM8 [Homo sapiens] >gi 6841450 gb AAF29078.1 AF161463_1 (AF161463) HSPC114 [Homo sapiens] (AJ000016) Cks1 protein [Arabidopsis thaliana] >gi 4510420 gb AAD21506.1 (AC006929) putative cyclin-dependent kinase regulatory subunit [Arabidopsis thaliana]
2542	LIB3602-041-Q6-K1-G1	2160174	BLASTX	572	8.00E-59	62	(AC000132) Identical to A. thaliana PUR2 (gb X74766). ESTs gb ATTS3927,gb N96446 come from this gene. [Arabidopsis thaliana]
2543	LIB3602-106-Q1-K1-H11	5281051	BLASTX	296	2.00E-26	49	(AL080318) stress-induced protein sti1-like protein [Arabidopsis thaliana] >gi 7267942 emb CAB78283.1 (AL161534) stress-induced protein sti1-like protein [Arabidopsis thaliana]
2544	LIB3602-062-Q6-K1-G6	7288201	BLASTX	320	3.00E-29	68	(AF108451) phosphoglycerate kinase precursor [Phaeodactylum tricornutum]
2545	LIB3602-066-Q1-K6-E1	7305087	BLASTX	394	6.00E-38	54	glutamine fructose-6-phosphate transaminase 2 >gi 6226821 sp Q9Z2Z9 GFA2_MOUSE GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] 2 (HEXOSEPHOSPHATE AMINOTRANSFERASE 2) (D-FRUCTOSE-6-PHOSPHATE AMIDOTRANSFERASE 2) (GFAT 2) (GFAT2) >gi 4239879
2546	LIB3602-053-Q6-K1-A9	7490623	BLASTX	185	1.00E-13	45	heat shock protein 70 family - fission yeast (Schizosaccharomyces pombe) >gi 2992154 dbj BAA25322.1 (AB012387) heat shock protein [Schizosaccharomyces pombe] >gi 3581889 emb CAA20787.1 (AL031540) heat shock protein 70 family [Schizosaccharomyces pombe]
2547	LIB3602-016-Q6-K1-F3	4826940	BLASTX	156	8.00E-15	40	Pro-X carboxypeptidase precursor >gi 1172047 sp P42785 PCP_HUMAN LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR (PROLYLCARBOXYPEPTIDASE) (PRCP) (PROLINE CARBOXYPEPTIDASE) (ANGIOTENSINASE C) (LYSOSOMAL CARBOXYPEPTIDASE C) >gi 476943 pir A47352 lysosomal Pro-X
2548	LIB3602-048-Q6-K1QA-D10	3219858	BLASTX	245	1.00E-20	45	DNA-DIRECTED RNA POLYMERASE II 13.6 KD POLYPEPTIDE >gi 2129724 pir S71204 DNA-directed RNA polymerase (EC 2.7.7.6) II 13.6K chain - Arabidopsis thaliana >gi 881501 gb AAB02849.1 (U28048) RNA polymerase II 13.6 kDa subunit [Arabidopsis thaliana] >gi 4678
2549	LIB3602-022-Q6-K1-D12	7435799	BLASTX	317	4.00E-29	46	cysteine proteinase (EC 3.4.22.-) - barley >gi 2224810 emb CAB09698.1 (Z97022) cysteine proteinase [Hordeum vulgare]
2550	LIB3602-023-Q6-K1-H2	2213612	BLASTX	201	2.00E-15	40	(AC000103) F21J9.6 [Arabidopsis thaliana]
2551	LIB3602-010-Q6-K1-E7	4512684	BLASTX	265	7.00E-23	61	(AC006931) unknown protein [Arabidopsis thaliana]
2552	LIB3602-042-Q6-K1-A5	6692118	BLASTX	570	1.00E-58	89	(AC007764) F22C12.2 [Arabidopsis thaliana]
2553	LIB3602-054-Q6-K1-A10	5921971	BLASTX	469	7.00E-47	55	(AF106575) contains similarity to Pfam domain PF00171 (aldehyd), Score=286.5, E-value=1.1e-82,

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2554	LIB3602-062-Q6-K1-H1	7267544	BLASTX	649	7.00E-68	64	N=1 [Caenorhabditis elegans] (AL161513) isoamylase-like protein [Arabidopsis thaliana]
2555	LIB3602-064-Q1-K6-G11	4679028	BLASTX	145	1.00E-08	28	(AF077207) HSPC021 [Homo sapiens] >gi 5106781 gb AAD39841.1 (AF083243) HSPC025 [Homo sapiens]
2556	LIB3602-022-Q6-K1-B1	6735297	BLASTX	290	6.00E-26	42	(AL137080) putative protein [Arabidopsis thaliana]
2557	LIB3602-116-Q1-K1-A11	2500352	BLASTX	300	6.00E-46	58	60S RIBOSOMAL PROTEIN L10 >gi 1129139 emb CAA63831.1 (X94087) similar to a gene located in region Xq27-28 of humans [Euglena gracilis]
2558	LIB3602-060-Q6-K1-D2	464980	BLASTX	436	5.00E-43	55	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 166422 gb AAA18528.1 (L06967) ubiquitin carrier protein [Medicago sativa]
2559	LIB3602-040-Q6-K1-D7	6754506	BLASTX	188	7.00E-14	35	like-glycosyltransferase >gi 3954978 emb CAA06945.1 (AJ006278) acetylglucosaminyltransferase-like protein [Mus musculus]
2560	LIB3602-047-Q6-K1-F9	7486019	BLASTX	227	2.00E-18	62	hypothetical protein F23E12.190 - Arabidopsis thaliana >gi 3080425 emb CAA18744.1 (AL022604) putative protein [Arabidopsis thaliana] >gi 7270477 emb CAB80242.1 (AL161587) putative protein [Arabidopsis thaliana]
2561	LIB3602-076-Q6-K6-B12	7428834	BLASTX	218	4.00E-18	68	probable P-glycoprotein pgp1 - Arabidopsis thaliana >gi 3355477 gb AAC27839.1 (AC004218) putative ABC transporter [Arabidopsis thaliana]
2562	LIB3602-038-Q6-K1-G6	6580769	BLASTX	346	2.00E-32	67	(AF088897) formate acetyltransferase [Zymomonas mobilis]
2563	LIB3602-034-Q6-K1-E5	7020000	BLASTX	169	1.00E-11	41	(AK000120) unnamed protein product [Homo sapiens]
2564	LIB3602-059-Q6-K1-A3	421929	BLASTX	568	1.00E-58	85	polyubiquitin - tomato >gi 312160 emb CAA51679.1 (X73156) ubiquitin [Lycopersicon esculentum]
2565	LIB3602-092-Q6-K6-B3	296593	BLASTN	260	1.00E-144	94	H. vulgare pZE40 gene
2566	LIB3602-063-Q1-K6-E5	3450955	BLASTX	267	2.00E-23	72	(AF020736) ATPase homolog [Homo sapiens]
2567	LIB3602-048-Q6-K1QA-D7	2341033	BLASTX	451	1.00E-44	55	(AC000104) Similar to Babesia aldo-keto reductase (gb M93122). [Arabidopsis thaliana]
2568	LIB3602-023-Q6-K1-A8	7488984	BLASTX	163	6.00E-11	39	dem protein - tomato >gi 2190419 emb CAA73973.1 (Y13632) dem [Lycopersicon esculentum]
2569	LIB3602-011-Q6-K1-D8	3024430	BLASTX	321	2.00E-29	43	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi 1928962 gb AAC14482.1 (U92287) pyrroline-5-carboxylate reductase [Actinidia deliciosa]
2570	LIB3602-101-Q1-K1-B3	1351139	BLASTX	224	4.00E-35	51	SUCROSE SYNTHASE ISOFORM I (SUCROSE-UDP GLUCOSYLTRANSFERASE I) (SUSY*DC1) >gi 480971 pir S37560 sucrose synthase (EC 2.4.1.13) - carrot >gi 406317 emb CAA53081.1 (X75332) sucrose synthase [Daucus carota] >gi 2760539 emb CAA76056.1 (Y16090) sucrose synt
2571	LIB3602-111-Q1-K1-G11	2493127	BLASTX	860	1.00E-92	96	VACUOLAR ATP SYNTHASE SUBUNIT B ISOFORM 1 (V-ATPASE B SUBUNIT)

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2572	LIB3602-011-Q6-K1-D3	4508082	BLASTX	329	2.00E-30	83	>gi 1303677 dbj BAA09099.1 (D50530) adenosine triphosphatase B subunit [Acetabularia acetabulum] (AC005882) Putative RNA polymerase II subunit Rpb10 [Arabidopsis thaliana]
2573	LIB3602-072-Q1-K1-D12	3182922	BLASTX	615	7.00E-64	72	ADP-RIBOSYLATION FACTOR 1
2574	LIB3602-071-Q1-K1-D10	6503190	BLASTX	184	2.00E-13	40	>gi 1654142 gb AAB17725.1 (U38470) small GTP-binding protein ARF [Brassica rapa] (AF200688) tyrosine kinase ZAK1 [Dictyostelium discoideum]
2575	LIB3602-016-Q6-K1-B11	4309741	BLASTX	233	3.00E-19	38	(AC006439) hypothetical protein [Arabidopsis thaliana]
2576	LIB3602-053-Q6-K1-D10	1076202	BLASTX	217	3.00E-17	44	calcium-stimulated protein kinase - Chlamydomonas eugametos
2577	LIB3602-113-Q1-K1-A10	1071912	BLASTX	410	3.00E-51	49	>gi 806542 emb CAA89202.1 (Z49233) calcium-stimulated protein kinase [Chlamydomonas eugametos]
2578	LIB3602-054-Q6-K1-A7	82056	BLASTX	258	4.00E-22	36	cysteine synthase (EC 4.2.99.8) cpACS1 - Arabidopsis thaliana >gi 572517 emb CAA57344.1 (X81698) cysteine synthase [Arabidopsis thaliana]
2579	LIB3602-109-Q1-K1-H10	7440340	BLASTX	415	4.00E-43	79	protein kinase, calcium-dependent (EC 2.7.1.-) - carrot (fragment)
2580	LIB3602-005-Q1-K1-D5	2854202	BLASTX	243	2.00E-20	35	ribosomal protein S14, cytosolic - Arabidopsis thaliana >gi 4886269 emb CAB43407.1 (AL050300) putative ribosomal protein S14 [Arabidopsis thaliana]
2581	LIB3602-086-Q6-K1-F10	2854203	BLASTX	197	7.00E-15	40	(AF045646) contains similarity to enol-CoA hydratases [Caenorhabditis elegans]
2582	LIB3602-053-Q6-K1-C2	99600	BLASTX	301	4.00E-27	78	(AF045646) contains similarity to the human polyposis locus-encoded protein (SW:Q00765) [Caenorhabditis elegans]
2583	LIB3602-029-Q6-K1-A11	462079	BLASTX	393	7.00E-38	64	chlorophyll a/b-binding protein - upland cotton
2584	LIB3602-032-Q6-K1-A11	7488014	BLASTX	296	1.00E-26	63	FERREDOXIN PRECURSOR
2585	LIB3602-060-Q6-K1-H12	5729913	BLASTX	316	6.00E-29	49	>gi 7427604 pir FEKM ferredoxin [2Fe-2S] precursor, chloroplast - Chlamydomonas reinhardtii
2586	LIB3602-074-Q1-K1-A7	3182986	BLASTX	222	8.00E-18	34	>gi 409202 gb AAA33085.1 (L10349) ferredoxin [Chlamydomonas reinhardtii]
2587	LIB3602-085-Q6-K1-C7	6646754	BLASTX	446	5.00E-44	50	>gi 1009714 gb AAC49171.1 (U29516) ferredoxin precursor [Chlamydomonas reinhardtii]
2588	LIB3602-051-Q6-K1-E4	7486079	BLASTX	317	3.00E-29	56	photosystem II protein W homolog T5F17.110 - Arabidopsis thaliana
							>gi 7269721 emb CAB81454.1 (AL161573) photosystem II protein W-like [Arabidopsis thaliana]
							mannosidase, alpha, class 1A, member 2
							>gi 3127047 gb AAC26169.1 (AF027156) alpha 1,2-mannosidase IB [Homo sapiens]
							PUTATIVE TRANSLATION INITIATION FACTOR EIF-2B SUBUNIT 2 (EIF-2B GDP-GTP EXCHANGE FACTOR) >gi 7447866 pir D69504 translation initiation factor eIF-2B, subunit delta (eif2BD) homolog - Archaeoglobus fulgidus
							>gi 2648498 gb AAB89217.1 (AE000962) translation
							(AC013258) unknown protein [Arabidopsis thaliana]
							hypothetical protein F24J7.100 - Arabidopsis thaliana >gi 2853081 emb CAA16931.1

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							(AL021768) ATP binding protein-like [Arabidopsis thaliana] >gi 7268750 emb CAB78956.1 (AL161551) ATP binding protein-like [Arabidopsis thaliana]
2589	LIB3602-014-Q6-K1-A10	4585874	BLASTX	487	3.00E-49	75	(AC005850) 60s ribosomal protein L3 [Arabidopsis thaliana]
2590	LIB3602-102-Q1-K1-H7	5669169	BLASTX	150	1.00E-16	75	(AF157017) photosystem I reaction center subunit V precursor [Tortula ruralis]
2591	LIB3602-014-Q6-K1-C2	5903045	BLASTX	550	3.00E-56	67	(AC008016) Similar to gb AF108945 signal peptidase 18 kDa subunit from Homo sapiens. ESTs gb H76629, gb H76949 and gb H76216 come from this gene. [Arabidopsis thaliana]
2592	LIB3602-102-Q1-K1-G5	7459514	BLASTX	246	1.00E-20	37	conserved hypothetical protein aq_1088 - Aquifex aeolicus >gi 2983568 gb AAC07141.1 (AE000722) hypothetical protein [Aquifex aeolicus]
2593	LIB3602-055-Q6-K1-H1	7529742	BLASTX	246	1.00E-20	61	(AL163527) 3-isopropylmalate dehydratase-like protein (small subunit) [Arabidopsis thaliana]
2594	LIB3602-001-P1-K6-D2	4886307	BLASTX	816	2.00E-87	84	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]
2595	LIB3602-030-Q6-K1-B2	7492644	BLASTX	178	9.00E-13	29	probable helicase - fission yeast (Schizosaccharomyces pombe) >gi 3116120 emb CAA18870.1 (AL023287) SNF2 family dna repair protein by similarity [Schizosaccharomyces pombe]
2596	LIB3602-023-Q6-K1-G3	7487137	BLASTX	220	1.00E-17	67	hypothetical protein T18B16.20 - Arabidopsis thaliana >gi 2832633 emb CAA16762.1 (AL021711) putative protein [Arabidopsis thaliana] >gi 7268700 emb CAB78907.1 (AL161550) putative protein [Arabidopsis thaliana]
2597	LIB3602-092-Q6-K6-G7	7447935	BLASTX	756	2.00E-80	86	probable potassium channel beta chain - rice >gi 1197587 gb AAC50046.1 (U46758) potassium channel beta subunit protein [Oryza sativa]
2598	LIB3602-049-Q6-K1-F7	3928891	BLASTX	415	1.00E-40	72	(AF093617) chlorophyll a/b binding protein [Acetabularia acetabulum]
2599	LIB3602-040-Q6-K1-G11	7484622	BLASTX	525	2.00E-53	74	L-ascorbate peroxidase (EC 1.11.1.11) precursor, stromal - common ice plant >gi 3202026 gb AAC19394.1 (AF069316) stromal L-ascorbate peroxidase precursor [Mesembryanthemum crystallinum]
2600	LIB3602-064-Q1-K6-A8	5903046	BLASTX	243	3.00E-20	64	(AC008016) F6D8.19 [Arabidopsis thaliana]
2601	LIB3602-025-Q6-K1-D12	1402884	BLASTX	660	3.00E-69	72	(X98130) unknown [Arabidopsis thaliana] >gi 1495265 emb CAA66120.1 (X97488) beta-transducin like protein [Arabidopsis thaliana]
2602	LIB3602-053-Q6-K1-F10	7486400	BLASTX	324	5.00E-30	55	hypothetical protein F4B14.80 - Arabidopsis thaliana >gi 3805847 emb CAA21467.1 (AL031986) putative protein [Arabidopsis thaliana] >gi 7270533 emb CAB81490.1 (AL161588) putative protein [Arabidopsis thaliana]
2603	LIB3602-094-Q6-K6-E7	131225	BLASTX	210	2.00E-16	40	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi 100605 pir A39759 photosystem I 18K protein precursor - barley >gi 167087 gb AAA62700.1 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]
2604	LIB3602-022-Q6-K1-G2	7493530	BLASTX	254	1.00E-21	43	trp-asp repeat protein - fission yeast (Schizosaccharomyces pombe)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2605	LIB3602-057-Q6-K1-G1	6094048	BLASTX	226	7.00E-36	75	>gi 5706505 emb CAB52267.1 (AL109739) trp-asp repeat protein [Schizosaccharomyces pombe] 60S RIBOSOMAL PROTEIN L30 >gi 2879811 emb CAA11256.1 (AJ223316) ribosomal protein L30 [Lupinus luteus]
2606	LIB3602-027-Q6-K1-C3	4193382	BLASTX	311	3.00E-28	86	(AF083336) ribosomal protein S27 [Arabidopsis thaliana] >gi 4193384 gb AAD10030.1 (AF083337) ribosomal protein S27 [Arabidopsis thaliana]
2607	LIB3602-006-Q1-K1-B8	6319146	BLASTX	219	2.00E-17	89	(AF193345) H2A protein [Oryza sativa]
2608	LIB3602-103-Q1-K1-D3	1708781	BLASTX	643	3.00E-67	73	(X97729) LMP7-like protein [Botryllus schlosseri]
2609	LIB3602-013-Q6-K1-H9	7295382	BLASTX	148	2.00E-09	54	(AE003564) CG10467 gene product [Drosophila melanogaster]
2610	LIB3602-054-Q6-K1-D1	6850936	BLASTX	169	7.00E-12	80	(AJ271667) putative proteasome regulatory subunit [Cicer arietinum]
2611	LIB3602-044-Q6-K1-E12	7294816	BLASTX	540	3.00E-55	67	(AE003547) hay gene product [Drosophila melanogaster]
2612	LIB3602-069-Q1-K1-B7	7529717	BLASTX	706	2.00E-74	72	(AL132969) fructose bisphosphate aldolase-like protein [Arabidopsis thaliana]
2613	LIB3602-005-Q1-K1-F2	7384808	BLASTX	335	5.00E-31	57	(AB040503) cysteine synthase [Allium tuberosum]
2614	LIB3602-042-Q6-K1-C6	7296277	BLASTX	200	3.00E-15	36	(AE003590) CG2761 gene product [Drosophila melanogaster]
2615	LIB3602-006-Q1-K1-D9	128825	BLASTX	415	2.00E-40	51	NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR (COMPLEX I-75KD) (CI-75KD) >gi 108830 pir A33552 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) 75K chain precursor - bovine >gi 163414 gb AAA30662.1 (J02877) NADH:ubiquinone reductase precursor [Bos]
2616	LIB3602-014-Q6-K1-F10	7025849	BLASTX	166	2.00E-11	38	(AC024128) hypothetical protein [Arabidopsis thaliana]
2617	LIB3602-066-Q1-K6-F7	7493333	BLASTX	308	5.00E-28	50	rna binding protein - fission yeast (Schizosaccharomyces pombe) >gi 3184100 emb CAA19313.1 (AL023777) putative RNA-binding protein [Schizosaccharomyces pombe]
2618	LIB3602-064-Q1-K6-B4	6721114	BLASTX	341	8.00E-32	59	(AC007396) T4O12.18 [Arabidopsis thaliana]
2619	LIB3602-049-Q6-K1-E9	4102582	BLASTX	198	4.00E-15	38	(AF013115) CAO [Arabidopsis thaliana]
2620	LIB3602-014-Q6-K1-E11	2501296	BLASTX	211	1.00E-16	61	DNA GYRASE SUBUNIT B >gi 7469301 pir S77162 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) chain B - Synechocystis sp. (strain PCC 6803) >gi 1652801 dbj BAA17720.1 (D90908) DNA gyrase B subunit [Synechocystis sp.]
2621	LIB3602-058-Q6-K1-A3	2088652	BLASTX	281	8.00E-25	37	(AF002109) 26S proteasome regulatory subunit [Arabidopsis thaliana] >gi 2351376 gb AAD03463.1 (U54561) translation initiation factor eIF2 p47 subunit homolog [Arabidopsis thaliana]
2622	LIB3602-073-Q1-K1-B5	3915037	BLASTX	355	2.00E-33	59	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 7433834 pir T06497 probable sucrose synthase (EC 2.4.1.13) 2 - garden pea >gi 2570067 emb CAA04512.1 (AJ001071) second sucrose synthase [Pisum sativum]
2623	LIB3602-012-Q6-K1-D2	6225722	BLASTX	202	2.00E-15	36	MRP PROTEIN HOMOLOG >gi 7446831 pir G70364 conserved hypothetical protein aq_737 - Aquifex aeolicus

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							>gi 2983325 gb AAC06915.1 (AE000705) hypothetical protein [Aquifex aeolicus]
2624	LIB3602-059-Q6-K1-H6	7440317	BLASTX	166	2.00E-17	66	ribosomal protein S14 - mouse
2625	LIB3602-022-Q6-K1-C3	6358788	BLASTX	449	2.00E-44	54	(AC010852) unknown protein [Arabidopsis thaliana]
2626	LIB3602-021-Q6-K1-C8	4581114	BLASTX	349	3.00E-33	69	(AC005825) putative HesB-like protein [Arabidopsis thaliana]
2627	LIB3602-018-Q6-K1-A3	3914161	BLASTX	175	2.00E-12	46	CYTOCHROME P450 55A2 (CYTOCHROME P450NOR1) >gi 1107453 dbj BAA11408.1 (D78511) cytochrome P450nor1 [Cylindrocarpum lichenicola]
2628	LIB3602-092-Q6-K6-H5	2492612	BLASTX	399	2.00E-38	73	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi 1076734 pir S52712 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) - rice >gi 755773 emb CAA59749.1 (X85747) 1-aminocyclopropane-1-carboxylate oxidase (A (AC024128) putative transporter [Arabidopsis thaliana]
2629	LIB3602-079-Q6-K6-B8	7025861	BLASTX	226	3.00E-18	29	PUTATIVE PRE-MRNA SPLICING FACTOR . ATP-DEPENDENT RNA HELICASE >gi 1402875 emb CAA66825.1 (X98130) RNA helicase [Arabidopsis thaliana] >gi 1495271 emb CAA66613.1 (X97970) RNA helicase [Arabidopsis thaliana]
2630	LIB3602-064-Q1-K6-G4	3913437	BLASTX	279	2.00E-24	75	(AF070942) ribulose-phosphate 3-epimerase transit form [Expression vector pFL505]
2631	LIB3602-071-Q1-K1-C12	3264790	BLASTX	241	5.00E-20	85	60S RIBOSOMAL PROTEIN L37A >gi 7441205 pir C71614 ribosomal protein L37A PFB0455w - malaria parasite (Plasmodium falciparum) >gi 3845189 gb AAC71880.1 (AE001396) ribosomal protein L37A [Plasmodium falciparum]
2632	LIB3602-120-Q1-K1-C12	6225908	BLASTX	144	4.00E-09	81	(AF085356) putative RNA helicase [Homo sapiens]
2633	LIB3602-018-Q6-K1-F12	5114047	BLASTX	351	4.00E-33	48	capreomycin acetyltransferase (EC 2.3.1.-) - Streptomyces capreolus >gi 1223838 gb AAA92035.1 (U13077) capreomycin acetyltransferase [Streptomyces capreolus] >gi 1586532 prf 2204233A capreomycin acetyltransferase [Streptomyces capreolus]
2634	LIB3602-079-Q6-K6-C6	2144171	BLASTX	156	5.00E-10	40	(AJ223384) 26S proteasome regulatory ATPase subunit 10b (S10b) [Manduca sexta]
2635	LIB3602-089-Q6-K6-G4	2960216	BLASTX	395	3.00E-44	66	hypothetical protein F27B13.100 - Arabidopsis thaliana >gi 4914410 emb CAB43661.1 (AL050352) putative protein [Arabidopsis thaliana]
2636	LIB3602-114-Q1-K1-F5	7486220	BLASTX	258	5.00E-22	43	>gi 7269885 emb CAB79744.1 (AL161575) putative protein [Arabidopsis thaliana]
2637	LIB3602-045-Q6-K1-B4	4758714	BLASTX	243	2.00E-20	40	microsomal glutathione S-transferase 3 >gi 7387731 sp O14880 GST3_HUMAN MICROSOMAL GLUTATHIONE S-TRANSFERASE 3 (MICROSOMAL GST-3) (MICROSOMAL GST-III) >gi 2583081 gb AAB82609.1 (AF026977) microsomal glutathione S-transferase 3 [Homo sapiens]
2638	LIB3602-017-Q6-K1-H9	4206112	BLASTX	208	1.00E-16	100	(AF097662) alpha tubulin [Mesembryanthemum

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2639	LIB3602-078-Q6-K6-E2	4586592	BLASTX	687	3.00E-72	68	crystallinum] (AB025000) multicatalytic endopeptidase complex [Cicer arietinum]
2640	LIB3602-119-Q1-K1-E8	7296284	BLASTX	255	1.00E-37	77	(AE003591) CG5605 gene product [alt 1] [Drosophila melanogaster]
2641	LIB3602-120-Q1-K1-B3	100596	BLASTX	157	3.00E-10	100	>gi 7296285 gb AAF51575.1 (AE003591) CG5605 gene product [alt 2] [Drosophila melanogaster]
2642	LIB3602-014-Q6-K1-G9	7543911	BLASTX	477	6.00E-48	70	metallothionein-like protein - barley
2643	LIB3602-078-Q6-K6-A7	7505775	BLASTX	226	8.00E-19	81	>gi 234815 gb AAB19699.1 (S53707) B22EL8 [Hordeum vulgare=barley, aleurone cells, Peptide, 115 aa] >gi 228182 prf 1718305A B22E protein [Hordeum vulgare]
2644	LIB3602-105-Q1-K1-A8	117519	BLASTX	642	6.00E-70	76	(AL163572) ubiquinol--cytochrome-c reductase-like protein [Arabidopsis thaliana]
2645	LIB3602-041-Q6-K1-F4	6598624	BLASTX	189	3.00E-14	68	hypothetical protein K11D2.3 - Caenorhabditis elegans
2646	LIB3602-102-Q1-K1-A10	5679842	BLASTX	206	5.00E-16	51	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)
2647	LIB3602-052-Q6-K1-F8	3024020	BLASTX	495	6.00E-50	75	>gi 99945 pir A39597 phytoene dehydrogenase (EC 1.3.-.-) - soybean >gi 170044 gb AAA34001.1 (M64704) phytoene desaturase [Glycine max]
2648	LIB3602-076-Q6-K6-A6	1213515	BLASTN	38	2.00E-11	89	(AC006837) putative ubiquinol-cytochrome c reductase [Arabidopsis thaliana]
2649	LIB3602-044-Q6-K1-F11	1708311	BLASTX	681	9.00E-72	83	(AJ243961) 11332.6 [Oryza sativa]
2650	LIB3602-004-Q1-K1-C9	6069644	BLASTX	157	2.00E-10	35	INITIATION FACTOR 5A-3 (EIF-5A) (EIF-4D) >gi 744351 pir T07133 translation initiation factor eIF-5A3 - potato >gi 2225881 dbj BAA20877.1 (AB004824) eukaryotic initiation factor 5A3 [Solanum tuberosum]
2651	LIB3602-047-Q6-K1-H9	7302323	BLASTX	419	5.00E-41	59	Gadus morhua ribosomal protein L22 mRNA, partial cds
2652	LIB3602-062-Q6-K1-D3	7267302	BLASTX	510	1.00E-51	61	CHLOROPLAST STROMA 70 KD HEAT SHOCK-RELATED PROTEIN
2653	LIB3602-104-Q1-K1-G11	1363492	BLASTX	353	4.00E-33	42	>gi 7441859 pir T09119 dnaK-type molecular chaperone HSP80 precursor, chloroplast - spinach (fragment) >gi 170094 gb AAA18570.1 (M99565) 80 kDa heat shock protein [Spinacia oleracea]
2654	LIB3602-019-Q6-K1-B2	7435702	BLASTX	243	1.00E-20	50	(AP000616) similar to Bacillus subtilis genome; unknown protein (Z99110) [Oryza sativa]
2655	LIB3602-003-Q1-K1-G1	2982322	BLASTX	471	5.00E-47	66	(AE003790) CG3358 gene product [Drosophila melanogaster]
2656	LIB3602-079-Q6-K6-F12	1345838	BLASTX	774	2.00E-82	75	(AL161503) UV-damaged DNA binding factor-like protein [Arabidopsis thaliana]
							outer envelope membrane protein OEP75 precursor - garden pea >gi 576507 gb AAA53275.1 (L36858) outer membrane protein [Pisum sativum]
							>gi 633607 emb CAA58720.1 (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]
							hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1653655 dbj BAA18567.1 (D90915) ATP-dependent Clp protease proteolytic subunit [Synechocystis sp.]
							(AF051246) probable proteasome subunit [Picea mariana]
							PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2657	LIB3602-005-Q1-K1-A6	5921735	BLASTX	305	2.00E-27	57	>gi 2130143 pir S65060 phytoene desaturase precursor - maize >gi 1051180 gb AAC12846.1 (U37285) phytoene desaturase [Zea mays] 10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) >gi 1519241 gb AAB07452.1 (U65890) 10 kDa chaperonin [Brassica napus]
2658	LIB3602-029-Q6-K1-G3	6831610	BLASTX	377	5.00E-36	57	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) >gi 2662188 dbj BAA23724.1 (AB009086) BBC1 protein [Chlamydomonas sp.] (AC006420) unknown protein [Arabidopsis thaliana]
2659	LIB3602-008-Q6-K1-A4	4584358	BLASTX	198	5.00E-15	45	Cockayne syndrome 1 protein >gi 3121917 sp Q13216 CSA_HUMAN COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA >gi 1362773 pir A57090 CSA protein - human >gi 975302 gb AAA82605.1 (U28413) CSA protein [Homo sapiens]
2660	LIB3602-029-Q6-K1-A9	4557467	BLASTX	167	2.00E-11	35	HISTONE H2A-IV >gi 99437 pir JQ0796 histone H2A.IV - Volvox carteri >gi 170658 gb AAA34249.1 (M31922) histone H2A-IV [Volvox carteri]
2661	LIB3602-015-Q6-K1-C6	121985	BLASTX	342	7.00E-32	71	40S RIBOSOMAL PROTEIN S4 >gi 7440142 pir T01187 ribosomal protein S4 type I - maize >gi 2331301 gb AAB66899.1 (AF013487) ribosomal protein S4 type I [Zea mays]
2662	LIB3602-087-Q6-K1-A12	3914899	BLASTX	233	4.00E-19	57	60S RIBOSOMAL PROTEIN L2 (L8) (RIBOSOMAL PROTEIN TL2) >gi 71078 pir R5TOL8 ribosomal protein L8, cytosolic - tomato >gi 19343 emb CAA45863.1 (X64562) ribosomal protein L2 [Lycopersicon esculentum]
2663	LIB3602-061-Q6-K1-C10	266944	BLASTX	633	4.00E-66	70	Chlamydomonas reinhardtii 21gr ribosomal protein S14 (CRY1) gene, complete cds
2664	LIB3602-071-Q1-K1-B9	463856	BLASTN	59	3.00E-24	97	THIOREDOXIN REDUCTASE 1 (NADPH-DEPENDENT THIOREDOXIN REDUCTASE 1) (NTR 1) >gi 468526 emb CAA80656.1 (Z23109) Thioredoxin reductase [Arabidopsis thaliana] (AB025969) NAD-dependent sorbitol dehydrogenase [Prunus persica]
2665	LIB3602-080-Q6-K6-G8	2500129	BLASTX	366	1.00E-34	72	(AC009519) FIN19.9 [Arabidopsis thaliana]
2666	LIB3602-068-Q1-K1-G1	7416846	BLASTX	190	5.00E-14	51	(AK001798) unnamed protein product [Homo sapiens]
2667	LIB3602-086-Q6-K1-E2	6633812	BLASTX	163	6.00E-11	36	(AL132975) mannose-1-phosphate guanylyltransferase-like protein [Arabidopsis thaliana]
2668	LIB3602-045-Q6-K1-H8	7023297	BLASTX	153	8.00E-10	37	(AL049730) Ribosomal protein L7Ae-like [Arabidopsis thaliana] >gi 7267962 emb CAB78303.1 (AL161534) Ribosomal protein L7Ae-like [Arabidopsis thaliana]
2669	LIB3602-028-Q6-K1-F2	7076802	BLASTX	563	7.00E-58	64	60S RIBOSOMAL PROTEIN L15-2 >gi 2982318 gb AAC32144.1 (AF051244) probable 60S ribosomal protein L15 [Picea mariana]
2670	LIB3602-022-Q6-K1-D6	5823571	BLASTX	265	6.00E-23	72	(AB034249) geranylgeranyl pyrophosphate synthase [Croton sublyratus]
2671	LIB3602-020-Q6-K1-B5	6093872	BLASTX	268	8.00E-24	73	(AF145311) 26S proteasome regulatory complex subunit p39A [Drosophila melanogaster]
2672	LIB3602-073-Q1-K1-B6	6277254	BLASTX	148	4.00E-09	59	
2673	LIB3602-035-Q1-K1-H10	6434960	BLASTX	324	9.00E-30	41	

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2674	LIB3602-008-Q6-K1-D2	6633814	BLASTX	174	2.00E-12	63	>gi 7301037 gb AAF56173.1 (AE003744) Rpn4 gene product [alt 1] [Drosophila melanogaster]
2675	LIB3602-046-Q6-K1-H4	7486788	BLASTX	279	1.00E-24	59	>gi 7301038 gb AAF56174.1 (AE003744) Rpn4 gene product [alt 2] [Drosophila melan (AC009519) FIN19.11 [Arabidopsis thaliana]
2676	LIB3602-026-Q6-K1-C5	4808539	BLASTX	185	2.00E-13	66	hypothetical protein M3E9.70 - Arabidopsis thaliana >gi 2982456 emb CAA18220.1 (AL022223) putative protein [Arabidopsis thaliana]
2677	LIB3602-048-Q6-K1QA-E12	6714389	BLASTX	324	5.00E-30	61	>gi 7269502 emb CAB79505.1 (AL161565) putative protein [Arabidopsis thaliana] (AF075700) putative glutathione synthetase; GSHS2 [Medicago truncatula]
2678	LIB3602-054-Q6-K1-H1	3024001	BLASTX	404	3.00E-39	52	(AC012393) hypothetical protein [Arabidopsis thaliana]
2679	LIB3602-105-Q1-K1-E4	2655889	BLASTX	251	3.00E-21	31	H(+)/HEXOSE COTRANSPORTER 2 (GALACTOSE-H+ SYMPORTER)
2680	LIB3602-053-Q6-K1-B3	7494794	BLASTX	175	3.00E-12	50	>gi 18043 emb CAA47323.1 (X66855) HUP2 [Chlorella kessleri] (AL009171) 62D9.b [Drosophila melanogaster]
2681	LIB3602-032-Q6-K1-C11	7484997	BLASTX	214	5.00E-17	50	hypothetical protein B0261.4 - Caenorhabditis elegans >gi 1938549 gb AAB52351.1 (U97016) similar to drosophila Rlc1 gene product (NID:g563361) and S. cerevisiae mitochondrial 60S ribosomal protein L4 (YML4) (NID:g459259) [Caenorhabditis elegans]
2682	LIB3602-072-Q1-K1-A4	2982311	BLASTX	561	2.00E-57	60	H+-transporting ATPase (EC 3.6.1.35) 14K chain, vacuolar - Arabidopsis thaliana >gi 3892056 gb AAC78269.1 AAC78269 (AC002330) putative vacuolar ATPase [Arabidopsis thaliana] >gi 7269022 emb CAB80755.1 (AL161494) putative vacuolar ATPase [Arabidopsis thal
2683	LIB3602-021-Q6-K1-E2	7229709	BLASTX	300	2.00E-27	65	(AF051240) probable ubiquitin-conjugating enzyme E2 [Picea mariana]
2684	LIB3602-070-Q1-K1-C7	7239500	BLASTX	231	6.00E-19	54	(AF237624) 80S ribosomal protein L31 [Perilla frutescens]
2685	LIB3602-106-Q1-K1-E10	3776023	BLASTX	230	6.00E-31	42	(AC012654) Contains similarity to the late embryogenesis abundant protein from Picea glauca gb L47115. ESTs gb AI992795 and gb T45309 come from this gene. [Arabidopsis thaliana]
2686	LIB3602-022-Q6-K1-F2	5924062	BLASTX	359	5.00E-34	51	(AJ010473) RNA helicase [Arabidopsis thaliana]
2687	LIB3602-102-Q1-K1-H11	4680713	BLASTX	398	2.00E-51	71	(AF158699) unknown [Burkholderia cepacia]
2688	LIB3602-059-Q6-K1-H4	7480237	BLASTX	145	8.00E-09	42	(AF132971) CGI-37 protein [Homo sapiens] >gi 5114055 gb AAD40195.1 (AF085360) HSPC031 [Homo sapiens]
2689	LIB3602-084-Q6-K1-F11	7248415	BLASTX	157	4.00E-10	34	hypothetical protein SCJ4.42c - Streptomyces coelicolor >gi 5738802 emb CAB52976.1 (AL109950) hypothetical protein [Streptomyces coelicolor A3(2)]
2690	LIB3602-020-Q6-K1-A1	1174745	BLASTX	571	6.00E-59	80	(AP001389) ESTs AU077873(S1878),D40121(S1878) correspond to a region of the predicted gene.~Similar to Arabidopsis thaliana 60S ribosomal protein L13 (P41127) [Oryza sativa]
							TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM) >gi 1363523 pir S53761 triose-phosphate isomerase

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							(EC 5.3.1.1) precursor, chloroplast - rye >gi 609262 emb CAA83533.1 (Z32521) triosephosphate isomerase [Secale cereale] >gi 1095494 prf 2109226B tr
2691	LIB3602-050-Q6-K1-C9	2982305	BLASTX	339	1.00E-31	73	(AF051237) 60S ribosomal protein L3 [Picea mariana]
2692	LIB3602-039-Q6-K1-G9	3334374	BLASTX	171	9.00E-12	85	TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA SEQUENCE-BINDING PROTEIN) (TBP) >gi 2708495 gb AAC49985.1 (U95549) TATA-binding protein [Candida albicans] >gi 2708497 gb AAC49986.1 (U95550) TATA-binding protein [Candida albicans]
2693	LIB3602-045-Q6-K1-G11	4567249	BLASTX	251	3.00E-21	45	(AC007070) hypothetical protein [Arabidopsis thaliana]
2694	LIB3602-002-P1-K6-E4	6174939	BLASTX	191	6.00E-15	81	60S RIBOSOMAL PROTEIN L37-B (YL27) >gi 2275274 gb AAB63862.1 (U97370) 60S ribosomal protein homolog [Schizosaccharomyces pombe]
2695	LIB3602-101-Q1-K1-C6	121966	BLASTX	265	7.00E-23	69	HISTONE H2A.1 >gi 70689 pir HSXLA1 histone H2A.1 - African clawed frog >gi 64777 emb CAA26817.1 (X03018) histone H2A (aa 1-130) [Xenopus laevis] >gi 214284 gb AAA49769.1 (M21287) histone H2A [Xenopus laevis]
2696	LIB3602-013-Q6-K1-E3	6919944	BLASTX	477	1.00E-47	61	PROBABLE 26S PROTEASOME REGULATORY SUBUNIT S12 (MOV34 PROTEIN) >gi 2351374 gb AAD03464.1 (U54560) putative 26S proteasome subunit athMOV34 [Arabidopsis thaliana]
2697	LIB3602-073-Q1-K1-F12	7469855	BLASTX	258	5.00E-22	37	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1652591 dbj BAA17512.1 (D90906) chloroplast import-associated channel IAP75 [Synechocystis sp.]
2698	LIB3602-005-Q1-K1-A3	7486947	BLASTX	140	8.00E-09	64	hypothetical protein T13E15.7 - Arabidopsis thaliana >gi 2344892 gb AAC31832.1 (AC002388) unknown protein [Arabidopsis thaliana]
2699	LIB3602-062-Q6-K1-E2	7487839	BLASTX	573	5.00E-59	63	hypothetical protein T9A14.170 - Arabidopsis thaliana >gi 4490341 emb CAB38623.1 (AL035656) putative protein [Arabidopsis thaliana] >gi 7270872 emb CAB80552.1 (AL161594) putative protein [Arabidopsis thaliana]
2700	LIB3602-081-Q6-K6-A5	118236	BLASTX	164	5.00E-11	45	DIHYDRODIPICOLINATE SYNTHASE 1 PRECURSOR (DHDPS) >gi 68224 pir WZWTH7 dihydrodipicolinate synthase (EC 4.2.1.52) precursor (clone pDA17) - wheat >gi 170680 gb AAA34263.1 (M60598) dihydrodipicolinate synthase [Triticum aestivum]
2701	LIB3602-120-Q1-K1-D10	7437314	BLASTX	283	4.00E-25	50	peptidylprolyl isomerase (EC 5.2.1.8) - Synechocystis sp. (PCC 6803) >gi 1652923 dbj BAA17841.1 (D90909) peptidyl-prolyl cis-trans isomerase [Synechocystis sp.]
2702	LIB3602-107-Q1-K1-C2	1174592	BLASTX	606	5.00E-63	94	TUBULIN ALPHA-1 CHAIN >gi 2119270 pir S60233 tubulin alpha-1 chain - garden pea >gi 525332 gb AAA79910.1 (U12589) alpha-tubulin [Pisum sativum]
2703	LIB3602-025-Q6-K1-A7	3046907	BLASTX	300	4.00E-27	90	(AF019886) beta-tubulin [Onchocerca volvulus]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2704	LIB3602-086-Q6-K1-B12	4567243	BLASTX	285	4.00E-25	37	(AC007070) putative synaptobrevin [Arabidopsis thaliana]
2705	LIB3602-095-Q6-K6-C1	7509168	BLASTX	159	8.00E-11	65	hypothetical protein W09C5.1 - Caenorhabditis elegans >gi 3880592 emb CAB04941.1 (Z82077) cDNA EST EMBL:D72613 comes from this gene; cDNA EST EMBL:D75538 comes from this gene; cDNA EST EMBL:D74123 comes from this gene; cDNA EST yk289c10.5 comes from this
2706	LIB3602-115-Q1-K1-E4	3288823	BLASTX	236	2.00E-19	37	(AF063852) FUS5 [Arabidopsis thaliana]
2707	LIB3602-005-Q1-K1-D1	3288821	BLASTX	168	3.00E-12	76	(AF063901) alanine:glyoxylate aminotransferase; transaminase [Arabidopsis thaliana] >gi 4733989 gb AAD28669.1 AC007209_5 (AC007209) alanine-glyoxylate aminotransferase [Arabidopsis thaliana]
2708	LIB3602-054-Q6-K1-C2	6382535	BLASTX	196	6.00E-15	54	(AC011020) putative protein kinase [Arabidopsis thaliana]
2709	LIB3602-005-Q1-K1-H1	4506221	BLASTX	242	3.00E-21	45	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 >gi 7451897 pir JC6523 26s proteasom p55 protein - human >gi 1945611 dbj BAA19749.1 (AB003103) 26S proteasome subunit p55 [Homo sapiens]
2710	LIB3602-025-Q6-K1-C9	6831664	BLASTX	697	1.00E-73	87	40S RIBOSOMAL PROTEIN S5 >gi 7440226 pir T16965 ribosomal protein S5 - curled-leaved tobacco >gi 1620982 emb CAA70084.1 (Y08860) 40S ribosomal protein S5 [Nicotiana plumbaginifolia] (AC009177) unknown protein [Arabidopsis thaliana]
2711	LIB3602-020-Q6-K1-H7	6729038	BLASTX	314	8.00E-29	44	(AC008153) putative eukaryotic translation initiation factor 3 subunit [Arabidopsis thaliana]
2712	LIB3602-077-Q6-K6-E6	6006879	BLASTX	306	1.00E-27	60	(AC020580) hypothetical protein [Arabidopsis thaliana]
2713	LIB3602-029-Q6-K1-G10	7543738	BLASTX	241	4.00E-20	46	(AC020580) hypothetical protein [Arabidopsis thaliana]
2714	LIB3602-101-Q1-K1-G4	115791	BLASTX	210	1.00E-16	72	CHLOROPHYLL A-B BINDING PROTEIN 2 PRECURSOR (LHCII TYPE I CAB-2) (LHCP) >gi 81770 pir S01961 chlorophyll a/b-binding protein 2 precursor - soybean >gi 18548 emb CAA31418.1 (X12980) chlorophyll a/b binding preprotein (AA -33 to 223) [Glycine max]
2715	LIB3602-039-Q6-K1-D2	6598844	BLASTX	327	4.00E-30	44	(AC010795) hypothetical protein [Arabidopsis thaliana]
2716	LIB3602-116-Q1-K1-F1	115796	BLASTX	183	5.00E-14	79	CHLOROPHYLL A-B BINDING PROTEIN PRECURSOR (LHCII TYPE I CAB) (LHCP) >gi 218174 dbj BAA00537.1 (D00642) type II light-harvesting chlorophyll a/b-binding protein [Oryza sativa]
2717	LIB3602-095-Q6-K6-D3	4759036	BLASTX	167	3.00E-13	35	regucalcin (senescence marker protein-30) >gi 3334328 sp Q15493 SM30_HUMAN SENESCENCE MARKER PROTEIN-30 (SMP-30) (REGUCALCIN) (RC) >gi 2136176 pir I52491 SMP-30 - human >gi 7429379 pir S60035 senescence marker protein 30 - human >gi 1072312 dbj BAA06602
2718	LIB3602-046-Q6-K1-B1	7488941	BLASTX	668	3.00E-70	82	adenosylhomocysteinase (EC 3.3.1.1) - parsley >gi 169661 gb AAA33855.1 (M62756) S-adenosylhomocysteine hydrolase [Petroselinum crispum]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2719	LIB3602-045-Q6-K1-G7	6598834	BLASTX	618	2.00E-64	78	(AC010795) putative replication factor C [Arabidopsis thaliana]
2720	LIB3602-049-Q6-K1-F12	3023500	BLASTX	177	1.00E-12	63	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 2 (ENDOPEPTIDASE CLP 2) >gi 2351823 gb AAB68677.1 (U92039) ATP-dependent Clp protease, proteolytic subunit [Synechococcus PCC7942]
2721	LIB3602-014-Q6-K1-C12	6598677	BLASTX	192	2.00E-14	36	(AC007135) hypothetical protein [Arabidopsis thaliana]
2722	LIB3602-007-Q1-K1-F7	1710008	BLASTX	255	1.00E-21	53	GTP-BINDING NUCLEAR PROTEIN RAN1B >gi 1370205 emb CAA98188.1 (Z73960) RAN1B [Lotus japonicus]
2723	LIB3602-111-Q1-K1-D12	2501056	BLASTX	323	1.00E-29	48	SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) >gi 2129737 pir S71293 serine-tRNA ligase (EC 6.1.1.11) - Arabidopsis thaliana >gi 1359497 emb CAA94388.1 (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana]
2724	LIB3602-109-Q1-K1-E8	7491321	BLASTX	164	5.00E-11	32	hypothetical protein SPBC119.09c - fission yeast (Schizosaccharomyces pombe) >gi 2959370 emb CAA17924.1 (AL022117) hypothetical protein. [Schizosaccharomyces pombe]
2725	LIB3602-014-Q6-K1-E3	2501062	BLASTX	147	3.00E-09	43	THREONYL-TRNA SYNTHETASE (THREONINE--TRNA LIGASE) (THRRS) >gi 7437520 pir S76615 hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1001722 dbj BAA10559.1 (D64004) threonyl-tRNA synthetase [Synechocystis sp.]
2726	LIB3602-117-Q1-K1-H3	4210330	BLASTX	354	2.00E-33	55	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]
2727	LIB3602-018-Q6-K1-F1	4098989	BLASTX	194	2.00E-14	36	(U81498) phenylalkylamine binding protein homolog [Arabidopsis thaliana]
2728	LIB3602-061-Q6-K1-H2	4210334	BLASTX	314	9.00E-29	68	(AJ223804) 2-oxoglutarate dehydrogenase, E3 subunit [Arabidopsis thaliana]
2729	LIB3602-014-Q6-K1-B1	4432812	BLASTX	204	1.00E-15	34	(AC006593) putative cysteinyl-tRNA synthetase [Arabidopsis thaliana]
2730	LIB3602-023-Q6-K1-H7	5531416	BLASTX	355	2.00E-33	48	(AJ243758) translocon Tic40 [Pisum sativum]
2731	LIB3602-028-Q6-K1-C10	4049522	BLASTX	414	2.00E-40	75	(AJ011516) fructose-bisphosphate aldolase [Scherffelia dubia]
2732	LIB3602-073-Q1-K1-D5	2564066	BLASTX	143	8.00E-09	65	(D45900) LEDI-3 protein [Lithospermum erythrorhizon]
2733	LIB3602-081-Q6-K6-C9	2497858	BLASTX	209	3.00E-16	45	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi 7431169 pir T08077 malate dehydrogenase (EC 1.1.1.37) precursor, mitochondrial - Chlamydomonas reinhardtii >gi 1145722 gb AAA84971.1 (U40212) malate dehydrogenase [Chlamydomonas reinhardtii]
2734	LIB3602-100-Q1-K1-B11	6056206	BLASTX	211	6.00E-20	53	(AC009400) putative kinesin-like centromere protein [Arabidopsis thaliana]
2735	LIB3602-118-Q1-K1-H10	2149901	BLASTX	186	1.00E-13	51	(U94707) unknown [Enterococcus faecalis]
2736	LIB3602-018-Q6-K1-D2	6729045	BLASTX	163	6.00E-11	43	(AC009177) putative aminopeptidase [Arabidopsis thaliana]
2737	LIB3602-062-Q6-K1-C9	7447193	BLASTX	357	1.00E-33	43	conserved hypothetical protein aq_1660 - Aquifex aeolicus >gi 2983997 gb AAC07543.1 (AE000749) hypothetical protein [Aquifex aeolicus]
2738	LIB3602-111-Q1-K1-B6	132894	BLASTX	182	3.00E-13	58	CYANELLE 50S RIBOSOMAL PROTEIN L33 >gi 71357 pir R5KT33 ribosomal protein L33 -

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							Cyanophora paradoxa cyanelle >gi 11401 emb CAA35534.1 (X17498) L33 ribosomal protein (AA 1-64) [Cyanophora paradoxa] >gi 1016146 gb AAA81233.1 (U30821) ribosomal protein L3
2739	LIB3602-036-Q6-K1-H9	6978417	BLASTX	162	1.00E-10	30	(AC005941) L5204.2 [Leishmania major]
2740	LIB3602-010-Q6-K1-A11	963025	BLASTN	34	3.00E-09	93	D.hydei gene for histone H3.3B
2741	LIB3602-057-Q6-K1-E6	3929364	BLASTX	551	3.00E-56	84	NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I- 23KD) (CI-23KD) (COMPLEX I-28.5KD) (CI- 28.5KD) >gi 1076356 pir S52380 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain TYKY precursor - Arabidopsis thaliana >gi 666977 emb CAA59061.1 (X
2742	LIB3602-086-Q6-K1-B6	226263	BLASTX	154	8.00E-10	35	chlorophyll a/b binding protein [Glycine max]
2743	LIB3602-040-Q6-K1-C5	2500139	BLASTX	162	2.00E-11	56	PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1) >gi 7428981 pir S76914 translation releasing factor RF-1 - Synechocystis sp. (strain PCC 6803) >gi 1653916 dbj BAA18826.1 (D90917) peptide chain release factor [Synechocystis sp.] (AF054617) one helix protein [Arabidopsis thaliana] >gi 7340686 emb CAB82985.1 (AL162508) one helix protein (OHP) [Arabidopsis thaliana]
2744	LIB3602-042-Q6-K1-G3	3283057	BLASTX	163	5.00E-11	50	(AF149413) similar to malate dehydrogenases; Pfam PF00390, Score=1290.5. E=0, N=1 [Arabidopsis thaliana]
2745	LIB3602-016-Q6-K1-H7	5107826	BLASTX	219	1.00E-17	38	50S RIBOSOMAL PROTEIN L6 >gi 7440700 pir C72054 L6 ribosomal protein - Chlamydia pneumoniae (strain CWL029) >gi 4376931 gb AAD18772.1 (AE001647) L6 Ribosomal Protein [Chlamydomonas reinhardtii] >gi 7189048 gb AAF37997.1 (AE002173) ribosomal protein L6 [
2747	LIB3602-067-Q1-K1-B10	6715645	BLASTX	248	5.00E-21	66	(AC007323) T25K16.8 [Arabidopsis thaliana]
2748	LIB3602-051-Q6-K1-H12	7445539	BLASTX	276	2.00E-24	48	aldose 1-epimerase - Thermotoga maritima (strain MSB8) >gi 4980780 gb AAD35370.1 AE001710_5 (AE001710) aldose 1-epimerase [Thermotoga maritima]
2749	LIB3602-057-Q6-K1-A12	4325370	BLASTX	673	1.00E-70	63	(AF128396) similar to human phosphotyrosyl phosphatase activator PTPA (GB:X73478) [Arabidopsis thaliana] >gi 7267538 emb CAB78020.1 (AL161513) putative phosphotyrosyl phosphatase activator protein [Arabidopsis thaliana]
2750	LIB3602-017-Q6-K1-A11	5869803	BLASTX	257	6.00E-22	31	(X64418) kurz protein [Drosophila melanogaster]
2751	LIB3602-085-Q6-K1-B5	7301290	BLASTX	199	4.00E-15	42	(AE003751) CG11851 gene product [Drosophila melanogaster]
2752	LIB3602-051-Q6-K1-B11	7447302	BLASTX	165	3.00E-11	38	probable glutathione transferase (EC 2.5.1.18), 2,4- D inducible - soybean >gi 2920666 gb AAC18566.1 (AF048978) 2,4-D inducible glutathione S-transferase [Glycine max] (U56935) beta-1,3-glucanase IIa [Oerskovia xanthineolytica]
2753	LIB3602-109-Q1-K1-H7	1354764	BLASTX	145	4.00E-09	58	(AP000391) ESTs C22657(S0014),C22656(S0014) correspond to a region of the predicted gene.; Similar to receptor protein kinase, ERECTA
2754	LIB3602-043-Q6-K1-F5	5734642	BLASTX	153	6.00E-10	33	

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							(AC004484) [Oryza sativa] >gi 6006357 dbj BAA84787.1 (AP000559) ESTs C22657(S0014),C22656(S0014) correspond to a region
2755	LIB3602-012-Q6-K1-G7	3763918	BLASTX	573	6.00E-59	66	(AC004450) 3-isopropylmalate dehydratase, small subunit [Arabidopsis thaliana]
2756	LIB3602-040-Q6-K1-F6	6642738	BLASTX	191	3.00E-14	38	(AF113007) PRO0066 [Homo sapiens]
2757	LIB3602-064-Q1-K6-D6	4567273	BLASTX	383	1.00E-36	50	(AC006841) putative vacuolar proton-ATPase subunit 1 [Arabidopsis thaliana]
2758	LIB3602-117-Q1-K1-H10	3757515	BLASTX	204	8.00E-16	64	(AC005167) hypothetical protein [Arabidopsis thaliana]
2759	LIB3602-034-Q6-K1-B8	7385113	BLASTX	196	8.00E-15	43	(AF222766) ankyrin 1 [Bos taurus]
2760	LIB3602-047-Q6-K1-A4	7487883	BLASTX	218	2.00E-17	36	hypothetical protein T9J22.21 - Arabidopsis thaliana >gi 2739379 gb AAC14502.1 (AC002505) hypothetical protein [Arabidopsis thaliana]
2761	LIB3602-071-Q1-K1-C11	2500318	BLASTX	258	6.00E-22	63	50S RIBOSOMAL PROTEIN L28 >gi 7441051 pir S74715 ribosomal protein L28 - Synechocystis sp. (strain PCC 6803) >gi 1651940 dbj BAA16866.1 (D90901) 50S ribosomal protein L28 [Synechocystis sp.]
2762	LIB3602-068-Q1-K1-A10	7303420	BLASTX	435	1.00E-42	48	(AE003821) CG8778 gene product [Drosophila melanogaster]
2763	LIB3602-041-Q6-K1-B6	7510133	BLASTX	231	7.00E-19	59	hypothetical protein Y52B11A.3 - Caenorhabditis elegans >gi 3881161 emb CAA21721.1 (AL032654) similar to Heme-binding domain in cytochrome b5 and oxidoreductases [Caenorhabditis elegans]
2764	LIB3602-078-Q6-K6-E9	5281018	BLASTX	245	3.00E-21	63	(Z97339) OBP33pep like protein [Arabidopsis thaliana] >gi 7268299 emb CAB78594.1 (AL161541) OBP33pep like protein [Arabidopsis thaliana]
2765	LIB3602-077-Q6-K6-A10	1709243	BLASTX	254	7.00E-22	70	NUCLEOSIDE DIPHOSPHATE KINASE NBR-B (NDK NBR-B) (NDP KINASE NBR-B) >gi 4389319 pdb 1BE4 C Chain C, Nucleoside Diphosphate Kinase Isoform B From Bovine Retina >gi 1064897 emb CAA63533.1 (X92957) nucleoside-diphosphate kinase NBR-B [Bos taurus] (X77499) amino acid permease [Arabidopsis thaliana]
2766	LIB3602-032-Q6-K1-H11	3970652	BLASTX	148	2.00E-09	48	starch synthase DULL1 - maize >gi 3057120 gb AAC14014.1 (AF023159) starch synthase DULL1 [Zea mays]
2767	LIB3602-072-Q1-K1-E12	7489826	BLASTX	457	2.00E-45	51	(AE003556) CG7197 gene product [Drosophila melanogaster]
2768	LIB3602-066-Q1-K6-F5	7295126	BLASTX	436	7.00E-43	54	(AC009177) unknown protein [Arabidopsis thaliana]
2769	LIB3602-025-Q6-K1-D1	6729017	BLASTX	187	9.00E-14	48	(AB026909) F1-ATP synthase delta subunit [Ipomoea batatas]
2770	LIB3602-017-Q6-K1-C4	4774163	BLASTX	305	1.00E-27	36	ORIGIN RECOGNITION COMPLEX SUBUNIT 2 (XORC2) >gi 7512175 pir S68447 origin recognition complex chain orc2 - African clawed frog >gi 1177822 gb AAA96391.1 (U31984) XORC2 [Xenopus laevis]
2771	LIB3602-100-Q1-K1-D2	2498712	BLASTX	344	4.00E-32	47	>gi 1586824 prf 2204391A orc-2-related protein [Xenopus laevis]
2772	LIB3602-069-Q1-K1-E1	125577	BLASTX	318	5.00E-29	87	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							>gi 7434254 pir T08167 phosphoribulokinase (EC 2.7.1.19) precursor - Chlamydomonas reinhardtii
							>gi 167432 gb AAA33090.1 (M36123) phosphoribulokinase [Chlamydomonas reinhardtii]
							>gi 710740 (AJ249833) Acyl-CoA binding protein (ACBP) [Digitalis lanata]
2773	LIB3602-076-Q6-K6-B1	6002102	BLASTX	172	6.00E-12	45	(U97104) membrane transporter [Bactrocera tryoni]
2774	LIB3602-049-Q6-K1-C9	3676298	BLASTX	218	2.00E-17	35	(AJ248327) L3 Ribosomal protein [Medicago sativa subsp. x varia]
2775	LIB3602-059-Q6-K1-G6	6688812	BLASTX	684	5.00E-72	71	hypothetical protein - Synechocystis sp. (strain PCC 6803) >gi 1001355 dbj BAA10842.1 (D64006)
2776	LIB3602-119-Q1-K1-E3	7447939	BLASTX	171	9.00E-16	53	auxin-induced protein [Synechocystis sp.]
2777	LIB3602-007-Q1-K1-H9	320553	BLASTX	402	8.00E-39	62	anthranilate synthase (EC 4.1.3.27) alpha-2 chain - Arabidopsis thaliana
2778	LIB3602-015-Q6-K1-H4	2598039	BLASTX	255	1.00E-21	37	(AJ001273) manganese resistance 1 protein [Saccharomyces cerevisiae]
2779	LIB3602-078-Q6-K6-B3	124374	BLASTX	237	2.00E-19	34	ACETOLACTATE SYNTHASE (ACETOHYDROXY-ACID SYNTHASE) (ALS) >gi 96560 pir JC1218 acetolactate synthase (EC 4.1.3.18), FAD-independent - Klebsiella pneumoniae >gi 149211 gb AAA25079.1 (M73842)
2780	LIB3602-071-Q1-K1-G7	7487731	BLASTX	277	3.00E-24	47	acetolactate synthase [Klebsiella pneumoniae]
							hypothetical protein T5L19.160 - Arabidopsis thaliana >gi 4539006 emb CAB39627.1 (AL049481) putative protein [Arabidopsis thaliana]
							>gi 7267699 emb CAB78126.1 (AL161516) putative protein [Arabidopsis thaliana]
2781	LIB3602-057-Q6-K1-C8	7298683	BLASTX	160	2.00E-14	73	(AE003666) CG2493 gene product [Drosophila melanogaster]
2782	LIB3602-023-Q6-K1-D3	2130089	BLASTX	159	2.00E-10	55	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi 1100743 dbj BAA08105.1 (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]
2783	LIB3602-071-Q1-K1-D11	6562261	BLASTX	154	7.00E-10	55	(AL132980) putative protein [Arabidopsis thaliana]
2784	LIB3602-012-Q6-K1-E7	6969002	BLASTX	155	7.00E-10	32	(AL139079) putative oxidoreductase [Campylobacter jejuni]
2785	LIB3602-011-Q6-K1-E10	7488455	BLASTX	341	8.00E-32	49	hydroxymethylpyrimidine kinase (EC 2.7.1.49) / thiamin-phosphate pyrophosphorylase (EC 2.5.1.3) - rape >gi 2746079 gb AAC31298.1 (AF015310) BTH1 [Brassica napus]
2786	LIB3602-010-Q6-K1-D7	7484895	BLASTX	172	6.00E-12	49	cytochrome P450 homolog F13P17.33 - Arabidopsis thaliana >gi 3128210 gb AAC26690.1 (AC004077) putative cytochrome P450 [Arabidopsis thaliana]
2787	LIB3602-009-Q6-K1-C8	6016183	BLASTX	478	7.00E-48	55	PHOTOSYSTEM II STABILITY/ASSEMBLY FACTOR HCF136 >gi 3559807 emb CAA75723.1 (Y15628) HCF136 protein [Arabidopsis thaliana]
2788	LIB3602-114-Q1-K1-B5	2190717	BLASTN	38	1.00E-11	82	Cloning vector pBI-GL, complete sequence
2789	LIB3602-067-Q1-K1-C10	5107528	BLASTX	167	2.00E-11	36	Probing The Substrate Specificity Of The Intracellular Brain Platelet-Activating Factor Acetylhydrolase
2790	LIB3602-041-Q6-K1-D8	6572215	BLASTX	247	1.00E-20	44	(Z83844) dJ37E16.5 (novel protein similar to nitrophenylphosphatases from various organisms) [Homo sapiens]
2791	LIB3602-050-Q6-K1-C6	2829532	BLASTX	268	3.00E-23	43	HYPOTHETICAL 48.5 KD PROTEIN RV1407

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							>gi 7445108 pir D70901 probable fmu protein - Mycobacterium tuberculosis (strain H37RV)
							>gi 1542915 emb CAB02186.1 (Z80108) fmu [Mycobacterium tuberculosis]
2792	LIB3602-090-Q6-K6-C4	127210	BLASTX	353	3.00E-33	69	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING] (MMSDH)
							>gi 281523 pir B42902 methylmalonate-semialdehyde dehydrogenase (acylating) (EC 1.2.1.27) - Pseudomonas aeruginosa (ATCC 15692)
							>gi 151362 gb AAA25891.1 (M84911) methylmalonate semialdehyde d
2793	LIB3602-102-Q1-K1-C5	7433831	BLASTX	187	4.00E-28	63	sucrose synthase (EC 2.4.1.13) T2H3.8 - Arabidopsis thaliana >gi 3377802 gb AAC28175.1 (AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis thaliana]
2794	LIB3602-027-Q6-K1-F2	6572072	BLASTX	154	7.00E-10	49	(AL133452) putative protein [Arabidopsis thaliana]
2795	LIB3602-107-Q1-K1-F6	2129826	BLASTX	194	2.00E-14	30	phragmoplastin 5 - soybean
							>gi 1218004 gb AAC49183.1 (U36430) SDL5A [Glycine max]
2796	LIB3602-100-Q1-K1-D8	1708059	BLASTX	309	8.00E-35	51	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
							>gi 481593 pir S38908 glutathione reductase (NADPH) (EC 1.6.4.2) - common tobacco (fragment) >gi 431955 emb CAA53925.1 (X76293) glutathione reductase (NADPH) [Nicotiana tabacum]
2797	LIB3602-006-Q1-K1-E11	7291436	BLASTX	151	1.00E-23	90	(AE003458) CG4046 gene product [Drosophila melanogaster]
2798	LIB3602-011-Q6-K1-E11	4028549	BLASTX	170	1.00E-11	27	(AF093690) ubiquitin hydrolase B [Dictyostelium discoideum]
2799	LIB3602-037-Q6-K1-G10	7434563	BLASTX	407	1.00E-39	56	aspartate kinase (EC 2.7.2.4) / homoserine dehydrogenase (EC 1.1.1.3) precursor - soybean (fragment) >gi 2970556 gb AAC05983.1 (AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]
2800	LIB3602-071-Q1-K1-E6	7021737	BLASTX	166	3.00E-11	60	(AC024081) hypothetical protein [Arabidopsis thaliana]
2801	LIB3602-077-Q6-K6-H11	4204793	BLASTX	474	2.00E-47	48	(U52079) P-glycoprotein [Solanum tuberosum]
2802	LIB3602-081-Q6-K6-A7	6006398	BLASTN	41	1.00E-13	86	Aspergillus niger mRNA for ribosomal protein S28 (rps28 gene)
2803	LIB3602-088-Q6-K6-D9	7508349	BLASTX	186	2.00E-20	54	hypothetical protein T23H2.6 - Caenorhabditis elegans >gi 2731374 gb AAC48203.1 (U80033) T23H2.6 gene product [Caenorhabditis elegans]
2804	LIB3602-010-Q6-K1-D12	6319917	BLASTX	151	7.00E-10	36	protein kinase; Ssk22p
							>gi 140530 sp P25390 SS22_YEAST SERINE/THREONINE PROTEIN KINASE SSK22
							>gi 83250 pir S19488 probable membrane protein YCR073c - yeast (Saccharomyces cerevisiae)
							>gi 1907212 emb CAA42271.1 (X59720) YCR073c, len:1314 [Saccharomyces c
2805	LIB3602-120-Q1-K1-A2	1076820	BLASTX	149	1.00E-09	96	phosphoglycerate mutase (EC 5.4.2.1) - maize
2806	LIB3602-087-Q6-K1-A5	7387793	BLASTX	206	6.00E-16	34	TRANSLATION INITIATION FACTOR IF-3
2807	LIB3602-043-Q6-K1-A10	99898	BLASTX	210	1.00E-16	48	DNA-directed RNA polymerase (EC 2.7.7.6) largest chain (isoform B1) - soybean (fragment)
2808	LIB3602-049-Q6-K1-F2	4733939	BLASTX	492	1.00E-49	71	(AF068686) geranylgeranyl hydrogenase [Glycine max]
2809	LIB3602-053-Q6-K1-B2	337930	BLASTX	402	4.00E-39	67	(M22146) scar protein [Homo sapiens]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2810	LIB3602-001-P1-K6-D8	7446109	BLASTX	265	9.00E-23	48	RNA helicase RH16 - Arabidopsis thaliana >gi 5123708 emb CAB45452.1 (AL079347) RNA helicase (RH16) [Arabidopsis thaliana] >gi 7270442 emb CAB80208.1 (AL161586) RNA helicase (RH16) [Arabidopsis thaliana]
2811	LIB3602-091-Q6-K6-F3	1262849	BLASTX	268	3.00E-23	76	(U51633) type 1 light-harvesting chlorophyll a/b-binding polypeptide [Pinus palustris]
2812	LIB3602-037-Q6-K1-B9	3914594	BLASTX	167	2.00E-11	65	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 6 PRECURSOR (RUBISCO SMALL SUBUNIT 6) >gi 2654375 emb CAA82266.1 (Z28640) ribulosebiphosphate carboxylase, small subunit [Acetabularia cliftonii]
2813	LIB3602-012-Q6-K1-B2	7434369	BLASTX	194	2.00E-14	44	calcium-dependent protein kinase (EC 2.7.1.-) - sweet potato >gi 1552214 dbj BAA13440.1 (D87707) calcium dependent protein kinase [Ipomoea batatas]
2814	LIB3602-013-Q6-K1-B11	7520797	BLASTX	228	1.00E-18	43	phosphate permease PAB0927 - Pyrococcus abyssi (strain Orsay) >gi 5458819 emb CAB50306.1 (AJ248287) phosphate permease [Pyrococcus abyssi]
2815	LIB3602-001-P1-K6-D7	7522579	BLASTX	188	5.00E-14	36	similar to S. cerevisiae sur1 protein - fission yeast (Schizosaccharomyces pombe) (fragment) >gi 2408057 emb CAB16259.1 (Z99165) similar to S. cerevisiae sur1 protein [Schizosaccharomyces pombe]
2816	LIB3602-111-Q1-K1-E5	6630689	BLASTX	453	5.00E-54	63	(AP000969) ESTs D39011(R0609), AU032023(R3215) correspond to a region of the predicted gene.; Similar to 26S proteasome, non-ATPase subunit. (Y13071) [Oryza sativa]
2817	LIB3602-070-Q1-K1-G5	6912238	BLASTX	334	7.00E-31	46	antioxidant enzyme B166 >gi 6103724 gb AAF03750.1 AF110731_1 (AF110731) antioxidant enzyme B166 [Homo sapiens]
2818	LIB3602-078-Q6-K6-D5	7489167	BLASTX	157	2.00E-10	94	nascent polypeptide associated complex alpha chain - common tobacco (fragment) >gi 1658271 gb AAB18266.1 (U74622) nascent polypeptide associated complex alpha chain [Nicotiana tabacum]
2819	LIB3602-077-Q6-K6-D10	628056	BLASTX	245	1.00E-20	70	FK506-binding protein - Botryllus schlosseri >gi 435471 emb CAA53594.1 (X76006) FK506-binding protein [Botryllus schlosseri]
2820	LIB3602-066-Q1-K6-F2	6679088	BLASTX	505	6.00E-51	72	nicotinamide nucleotide transhydrogenase >gi 6225774 sp Q61941 NNTM_MOUSE NAD(P) TRANSHYDROGENASE, MITOCHONDRIAL PRECURSOR (PYRIDINE NUCLEOTIDE TRANSHYDROGENASE) (NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE) >gi 1083428 pir S54876 NAD(P)+ transhydrogenase (
2821	LIB3602-028-Q6-K1-H1	4325041	BLASTX	219	2.00E-17	66	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]
2822	LIB3602-120-Q1-K1-H2	6273391	BLASTX	221	8.00E-18	59	(AF196333) nonhistone protein 6 [Candida albicans]
2823	LIB3602-046-Q6-K1-E7	1175367	BLASTX	255	9.00E-22	63	HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I >gi 2130371 pir S58146 hypothetical protein SPAC2F7.02c - fission yeast (Schizosaccharomyces pombe)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							>gi 7491051 pir T38550 hypothetical protein SPAC2F7.02c - fission yeast (Schizosaccharomyces pombe)
2824	LIB3602-022-Q6-K1-A4	119002	BLASTX	247	7.00E-21	41	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE A1) >gi 80085 pir JQ0420 beta-1,3-glucanase A1 precursor - Bacillus circulans >gi 142973 gb AAA22474.1 (M34503) beta-1,3-glucanase A1 (glcA) [Bacillu
2825	LIB3602-007-Q1-K1-D8	1169128	BLASTX	160	1.00E-10	38	SERINE/THREONINE-PROTEIN KINASE CTR1 >gi 166680 gb AAA32779.1 (L08789) protein kinase [Arabidopsis thaliana] >gi 166682 gb AAA32780.1 (L08790) protein kinase [Arabidopsis thaliana] >gi 7340658 emb CAB82938.1 (AL162506) SERINE/THREONINE-PROTEIN KINASE C
2826	LIB3602-103-Q1-K1-E11	7298660	BLASTX	213	8.00E-17	45	(AE003665) CG10756 gene product [Drosophila melanogaster]
2827	LIB3602-092-Q6-K6-B7	7436158	BLASTX	246	2.00E-20	38	probable H ⁺ -transporting ATP synthase (EC 3.6.1.34) gamma chain, mitochondrial - Arabidopsis thaliana
2828	LIB3602-007-Q1-K1-F5	7433647	BLASTX	567	2.00E-58	69	acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor - cucurbit >gi 1694621 dbj BAA11117.1 (D70895) 3-ketoacyl-CoA thiolase [Cucurbita sp.] (Y09633) hypothetical protein [Bradyrhizobium japonicum]
2829	LIB3602-111-Q1-K1-B1	6433784	BLASTX	257	6.00E-22	36	(AF110781) photosystem I reaction center subunit PSAN precursor [Volvox carteri f. nagariensis]
2830	LIB3602-032-Q6-K1-B10	5902586	BLASTX	167	2.00E-11	49	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) (PP18) >gi 1777930 gb AAB40609.1 (U55019) nucleoside diphosphate kinase [Saccharum officinarum]
2831	LIB3602-059-Q6-K1-C2	2498077	BLASTX	167	9.00E-12	54	G box-binding protein homolog GBF1 - rape >gi 1399007 gb AAB03379.1 (U27108) transcription factor [Brassica napus]
2832	LIB3602-014-Q6-K1-F11	7488451	BLASTX	216	5.00E-17	52	NADH-UBIQUINONE OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD) (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi 346531 pir S28240 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-18(IP) precursor - bovine >gi 226 emb CAA44900.1 (X63215) NADH deh
2833	LIB3602-055-Q6-K1-F1	400578	BLASTX	216	3.00E-17	45	(AE002518) tRNA (uracil-5-)-methyltransferase [Neisseria meningitidis]
2834	LIB3602-057-Q6-K1-F6	7226932	BLASTX	266	5.00E-23	50	(AJ223326) DNA topoisomerase I [Daucus carota]
2835	LIB3602-077-Q6-K6-F7	5326994	BLASTX	310	4.00E-28	67	(AC019018) putative deoxyoctulononic acid synthetase [Arabidopsis thaliana]
2836	LIB3602-055-Q6-K1-G10	6862961	BLASTX	357	1.00E-33	70	PROBABLE COPPER-TRANSPORTING ATPASE SYNA >gi 79650 pir S10839 hypothetical protein 5 - Synechococcus sp. (PCC 6301) (fragment) >gi 48026 emb CAA29364.1 (X05925) VRF 5 (293 AA) [Synechococcus PCC6301]
2837	LIB3602-045-Q6-K1-C6	114718	BLASTX	179	7.00E-13	61	(AC002329) putative glucanase [Arabidopsis thaliana]
2838	LIB3602-050-Q6-K1-G1	6598335	BLASTX	234	2.00E-19	46	(AC007267) hypothetical protein [Arabidopsis thaliana]
2839	LIB3602-092-Q6-K6-H11	4662633	BLASTX	236	2.00E-19	35	

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2840	LIB3602-062-Q6-K1-B6	4510386	BLASTX	262	1.00E-22	53	(AC007017) unknown protein [Arabidopsis thaliana]
2841	LIB3602-029-Q6-K1-F1	6706420	BLASTX	710	4.00E-75	80	(AL133248) 40S ribosomal protein S2 homolog [Arabidopsis thaliana]
2842	LIB3602-044-Q6-K1-B8	6587806	BLASTX	187	8.00E-14	40	(AC010924) Contains similarity to gb M82916 MRS2 protein from Saccharomyces cerevisiae. ESTs gb N96043, gb AI998651, gb AA585850, gb T42027 come from this gene. [Arabidopsis thaliana]
2843	LIB3602-037-Q6-K1-A6	1076668	BLASTX	418	5.00E-41	75	NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) flavoprotein I precursor - potato >gi 639834 emb CAA58823.1 (X83999) NADH dehydrogenase [Solanum tuberosum]
2844	LIB3602-080-Q6-K6-F2	3024121	BLASTX	147	2.00E-09	60	S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 1724104 gb AAB38500.1 (U79767) methionine adenosyltransferase [Mesembryanthemum crystallinum]
2845	LIB3602-058-Q6-K1-D12	7300654	BLASTN	33	6.00E-09	90	Drosophila melanogaster genomic scaffold 142000013386035 section 57 of 105, complete sequence
2846	LIB3602-077-Q6-K6-D3	3334490	BLASTX	173	2.00E-12	66	DNA-DIRECTED RNA POLYMERASES I, II, AND III 7.3 KD POLYPEPTIDE (ABC10-ALPHA) >gi 7490493 pir T39794 DNA-directed RNA polymerases i, ii, and iii 7.3 kd polypeptide(abc10-alpha) - fission yeast (Schizosaccharomyces pombe) >gi 2529253 dbj BAA22807.1 (D8963
2847	LIB3602-111-Q1-K1-A6	7447234	BLASTX	181	5.00E-13	77	probable iron-sulfur cofactor synthesis protein F6H11.150 - Arabidopsis thaliana >gi 2827713 emb CAA16686.1 (AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana] >gi 6686815 emb CAB64727.1 (AJ243393) nifS-like p
2848	LIB3602-057-Q6-K1-E3	7437271	BLASTX	396	4.00E-38	64	UDPglucose 4-epimerase (EC 5.1.3.2) (clone GEPI42) - guar >gi 3021355 emb CAA06338.1 (AJ005081) UDP-galactose 4-epimerase [Cyanopsis tetragonoloba]
2849	LIB3602-030-Q6-K1-A10	2982272	BLASTX	256	6.00E-22	44	(AF051220) hypothetical protein [Picea mariana]
2850	LIB3602-054-Q6-K1-G10	6735326	BLASTX	377	4.00E-36	70	(AL137081) phenylalanine-tRNA synthetase-like protein [Arabidopsis thaliana]
2851	LIB3602-108-Q1-K1-C11	322386	BLASTX	158	1.00E-10	69	chlorophyll a/b-binding protein - green alga (Pyrobotrys stellata) >gi 18254 emb CAA49209.1 (X69434) a/b binding protein [Pyrobotrys stellata] (AF035293) similar to lysophospholipase [Homo sapiens]
2852	LIB3602-065-Q1-K6-A2	2661048	BLASTX	147	5.00E-09	36	
2853	LIB3602-114-Q1-K1-E11	1345933	BLASTX	350	2.00E-34	69	CITRATE SYNTHASE, GLYOXYSOMAL PRECURSOR (GCS) >gi 1084323 pir S53007 citrate synthase - cucurbit >gi 975633 dbj BAA07328.1 (D38132) glyoxysomal citrate synthase [Cucurbita sp.] (AF104631) light harvesting complex II protein precursor [Chlamydomonas reinhardtii]
2854	LIB3602-021-Q6-K1-G6	4139218	BLASTX	319	1.00E-29	68	
2855	LIB3602-114-Q1-K1-D5	2499503	BLASTX	478	1.00E-48	63	PHOSPHOGLYCERATE KINASE
2856	LIB3602-103-Q1-K1-A5	7506763	BLASTX	350	2.00E-45	72	hypothetical protein R166.2 - Caenorhabditis elegans >gi 3879192 emb CAA90663.1 (Z50795)

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							weak similarity with yeast cat8 regulatory protein (Swiss Prot accession number P39113); cDNA EST EMBL:Z14554 comes from this gene; cDNA EST EMBL:T02057 comes from t
2857	LIB3602-103-Q1-K1-A10	4389317	BLASTX	226	1.00E-18	66	Chain A, Nucleoside Diphosphate Kinase Isoform B From Bovine Retina >gi 4389318 pdb 1BE4 B Chain B, Nucleoside Diphosphate Kinase Isoform B From Bovine Retina
2858	LIB3602-027-Q6-K1-A5	4914683	BLASTX	239	8.00E-20	33	(AF067728) transactivating protein BRIDGE [Rattus norvegicus]
2859	LIB3602-046-Q6-K1-A7	7473075	BLASTX	305	4.00E-28	62	isocitrate lyase - Deinococcus radiodurans (strain R1) >gi 6458545 gb AAF10407.1 AE001937_3 (AE001937) isocitrate lyase [Deinococcus radiodurans]
2860	LIB3602-057-Q6-K1-D3	7436714	BLASTX	524	3.00E-53	69	acetolactate synthase (EC 4.1.3.18) - Chlamydomonas reinhardtii >gi 2906139 gb AAC03784.1 (AF047459) acetolactate synthase [Chlamydomonas reinhardtii]
2861	LIB3602-101-Q1-K1-H11	3882355	BLASTX	159	1.00E-10	72	(U92460) 12-oxophytodienoate reductase OPR1 [Arabidopsis thaliana] >gi 6143902 gb AAF04448.1 AC010718_17 (AC010718) 12-oxophytodienoate reductase (OPR1) [Arabidopsis thaliana]
2862	LIB3602-011-Q6-K1-H11	6648019	BLASTX	301	4.00E-27	39	HYPOTHETICAL 45.2 KD PROTEIN RV2685 >gi 7477890 pir [H70528 probable arsB protein - Mycobacterium tuberculosis (strain H37RV) >gi 2181976 emb CAB09476.1 (Z96072) arsB [Mycobacterium tuberculosis]
2863	LIB3602-055-Q6-K1-E4	7362763	BLASTX	401	7.00E-39	57	(AL162651) dTDP-glucose 4-6-dehydratase homolog D18 [Arabidopsis thaliana]
2864	LIB3602-115-Q1-K1-F6	7488693	BLASTX	545	1.00E-55	65	phosphate transport protein G7, mitochondrial - soybean >gi 3318611 dbj BAA31582.1 (AB016063) mitochondrial phosphate transporter [Glycine max]
2865	LIB3602-047-Q6-K1-E11	2500074	BLASTX	757	1.00E-80	89	GTP-BINDING PROTEIN YPTC4 >gi 1363474 pir [JC4106 GTP-binding protein yptC4 - Chlamydomonas reinhardtii >gi 806722 gb AAA82726.1 (U13167) YptC4 [Chlamydomonas reinhardtii]
2866	LIB3602-077-Q6-K6-E11	6686798	BLASTX	242	4.00E-20	43	(AJ242481) FKBP like protein [Arabidopsis thaliana]
2867	LIB3602-028-Q6-K1-D2	281003	BLASTX	148	3.00E-09	38	T-complex protein 10c (C3H allele) - mouse
2868	LIB3602-055-Q6-K1-E9	3962377	BLASTX	480	4.00E-48	57	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]
2869	LIB3602-064-Q1-K6-E5	2829916	BLASTX	160	2.00E-10	51	(AC002291) Unknown protein [Arabidopsis thaliana]
2870	LIB3602-004-Q1-K1-G11	7441896	BLASTX	415	2.00E-40	54	heat shock protein 90 homolog T22A6.20 - Arabidopsis thaliana >gi 5051761 emb CAB45054.1 (AL078637) HSP90-like protein [Arabidopsis thaliana] >gi 7269269 emb CAB79329.1 (AL161561) HSP90-like protein [Arabidopsis thaliana]
2871	LIB3602-063-Q1-K6-B1	7487954	BLASTX	155	4.00E-10	65	microfibril-associated protein homolog T15F16.8 - Arabidopsis thaliana >gi 2565010 gb AAB81880.1 AAB81880 (AC002983) putative microfibril-associated protein [Arabidopsis thaliana]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2872	LIB3602-019-Q6-K1-C6	2267084	BLASTX	149	3.00E-15	72	>gi 3377811 gb AAC28184.1 (AF076275) contains similarity to ATP synthase B (AF007889) calmodulin [Symbiodinium microadriaticum]
2873	LIB3602-068-Q1-K1-A2	7471620	BLASTX	185	2.00E-13	41	conserved hypothetical protein - Deinococcus radiodurans (strain R1)
2874	LIB3602-088-Q6-K6-H1	4416330	BLASTX	305	1.00E-27	70	>gi 6458247 gb AAF10133.1 AE001913_7 (AE001913) conserved hypothetical protein [Deinococcus radiodurans]
2875	LIB3602-003-Q1-K1-A10	464849	BLASTX	872	5.00E-94	93	(AF105295) S-adenosyl-homocysteine hydrolase like protein; SAHH-like protein [Alexandrium fundyense]
2876	LIB3602-108-Q1-K1-F2	461999	BLASTX	587	8.00E-61	81	TUBULIN ALPHA CHAIN >gi 486847 pir S36232 tubulin alpha chain - almond
2877	LIB3602-076-Q6-K6-H11	2982245	BLASTX	276	4.00E-24	49	>gi 20413 emb CAA47635.1 (X67162) alpha-tubulin [Prunus dulcis]
2878	LIB3602-029-Q6-K1-C6	322525	BLASTX	610	2.00E-63	69	ELONGATION FACTOR G, CHLOROPLAST PRECURSOR (EF-G)
2879	LIB3602-068-Q1-K1-G12	7327817	BLASTX	171	8.00E-12	32	(AF051205) hypothetical protein [Picea mariana]
2880	LIB3602-007-Q1-K1-G3	6651387	BLASTN	41	7.00E-14	84	omnipotent suppressor protein SUP1 homolog (clone A18) - Arabidopsis thaliana (fragment)
2881	LIB3602-104-Q1-K1-B10	7488813	BLASTX	278	2.00E-24	33	>gi 16512 emb CAA49171.1 (X69374) similar to yeast omnipotent suppressor protein SUP1 (SUP45); ORF [Arabidopsis thaliana]
2882	LIB3602-050-Q6-K1-C11	4375938	BLASTX	178	9.00E-13	44	(AL161946) putative protein [Arabidopsis thaliana]
2883	LIB3602-081-Q6-K6-F7	6677681	BLASTX	280	2.00E-47	52	Cloning vector pDDB57 complete sequence
2884	LIB3602-120-Q1-K1-D4	3915851	BLASTX	202	1.00E-15	61	import intermediate-associated 100K protein precursor - garden pea
2885	LIB3602-020-Q6-K1-F3	6911549	BLASTX	517	1.00E-52	87	>gi 1495768 emb CAA92823.1 (Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]
2886	LIB3602-054-Q6-K1-A4	4741966	BLASTX	206	5.00E-16	54	(AL031055) dH28H20.1 (similar to membrane transport protein) [Homo sapiens]
2887	LIB3602-007-Q1-K1-G5	7302240	BLASTX	344	5.00E-32	49	retinoblastoma binding protein 4
2888	LIB3602-051-Q6-K1-G12	7304024	BLASTX	178	1.00E-12	41	>gi 2494893 sp Q60972 RB48_MOUSE CHROMATIN ASSEMBLY FACTOR 1 P48 SUBUNIT (CAF-1 P48 SUBUNIT)
2889	LIB3602-011-Q6-K1-H1	1174844	BLASTX	278	2.00E-24	53	(RETINOBLASTOMA BINDING PROTEIN P48) (RETINOBLASTOMA-BINDING PROTEIN 4)
							>gi 2137734 pir I49366 G1/S transition control protein-b
							CHLOROPLAST 30S RIBOSOMAL PROTEIN S10 >gi 3603070 gb AAC35731.1 (AF041468)
							ribosomal protein S10 [Guillardia theta]
							(AJ249329) heat shock protein 70 [Cucumis sativus]
							(AF134133) Lil3 protein [Arabidopsis thaliana]
							(AE003787) CG10417 gene product [Drosophila melanogaster]
							(AE003836) CG14750 gene product [Drosophila melanogaster]
							UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (UBIQUITIN-PROTEIN LIGASE 2)
							(UBIQUITIN CARRIER PROTEIN 2)
							>gi 1076426 pir S43783 ubiquitin-conjugating enzyme UBC2 - Arabidopsis thaliana
							>gi 431264 gb AAA32899.1 (L19353) ubiquitin

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2890	LIB3602-079-Q6-K6-H2	7542542	BLASTX	221	1.00E-17	91	conjugating enzyme [Arabidopsis (AF238866) LNR42 [Mus musculus]
2891	LIB3602-035-Q1-K1-B8	7301359	BLASTX	145	7.00E-09	41	(AE003752) BcDNA:LD22548 gene product [Drosophila melanogaster]
2892	LIB3602-107-Q1-K1-E10	1346802	BLASTX	444	8.00E-44	60	PROFILIN 1 >gi 1076516 pir S49351 profilin 1 - kidney bean >gi 556836 emb CAA57508.1 (X81982) profilin [Phaseolus vulgaris]
2893	LIB3602-102-Q1-K1-D6	135099	BLASTX	447	2.00E-51	65	ASPARTYL-TRNA SYNTHETASE (ASPARTATE--TRNA LIGASE) (ASPRS) >gi 68531 pir SYRTDT aspartate--trna ligase (EC 6.1.1.12) - rat >gi 203066 gb AAA40789.1 (J04487) aspartyl-tRNA synthetase [Rattus norvegicus] >gi 1773257 gb AAC52981.1 (U30812) aspartyl-tRNA sy
2894	LIB3602-039-Q6-K1-A2	6437556	BLASTX	343	6.00E-32	38	(AC011623) unknown protein [Arabidopsis thaliana]
2895	LIB3602-027-Q6-K1-E11	3915866	BLASTX	404	3.00E-39	54	GLUTAMINYL-TRNA SYNTHETASE (GLUTAMINE--TRNA LIGASE) (GLNRS) >gi 7437754 pir T09643 glutamine--trna ligase (EC 6.1.1.18) - yellow lupine >gi 2995455 emb CAA62901.1 (X91787) tRNA-glutamine synthetase [Lupinus luteus]
2896	LIB3602-085-Q6-K1-B11	132917	BLASTX	189	2.00E-16	52	60S RIBOSOMAL PROTEIN L35 >gi 71362 pir R5RT35 ribosomal protein L35 - rat >gi 57702 emb CAA36001.1 (X51705) ribosomal protein L35 (AA 1-123) [Rattus rattus]
2897	LIB3602-036-Q6-K1-E6	3287875	BLASTX	170	1.00E-11	40	PROBABLE TETRAACYLDISACCHARIDE 4'-KINASE (LIPID A 4'-KINASE) >gi 290802 gb AAD15238.1 (L17003) valB gene product [Francisella tularensis var. novicida]
2898	LIB3602-038-Q6-K1-E10	115827	BLASTX	336	3.00E-31	80	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB) (LHCP) >gi 99383 pir A31392 chlorophyll a/b-binding protein - Chlamydomonas reinhardtii >gi 167409 gb AAA33082.1 (M24072) chlorophyll a/b-binding protein [Chlamydomonas reinhardtii]
2899	LIB3602-065-Q1-K6-B10	7441879	BLASTX	627	2.00E-65	79	dnaK-type molecular chaperone HSC70-11, mitochondrial - spinach >gi 2654212 gb AAB91473.1 (AF035458) heat shock 70 protein [Spinacia oleracea] >gi 2773052 gb AAB96660.1 (AF039084) heat shock 70 protein [Spinacia oleracea]
2900	LIB3602-016-Q6-K1-B10	7489392	BLASTX	216	3.00E-17	45	N-carbamyl-L-amino acid amidohydrolase homolog - barley (fragment) >gi 2695925 emb CAA10981.1 (AJ222776) hypothetical protein [Hordeum vulgare]
2901	LIB3602-036-Q6-K1-F2	1177368	BLASTN	33	5.00E-09	87	Z.mays mRNA for ribosomal protein L39
2902	LIB3602-102-Q1-K1-G6	4056502	BLASTX	183	2.00E-13	55	(AC005896) 40S ribosomal protein S5 [Arabidopsis thaliana]
2903	LIB3602-077-Q6-K6-C9	7301524	BLASTX	631	1.00E-65	61	(AE003758) CG6309 gene product [Drosophila melanogaster]
2904	LIB3602-017-Q6-K1-E5	6681113	BLASTX	259	3.00E-22	36	cytochrome P450, steroid inducible 3a11 >gi 5921911 sp Q64459 CP3B_MOUSE CYTOCHROME P450 3A11 (CYP11A11) (P-450IIAM1) (P-450UT) >gi 2117381 pir A60564 cytochrome P450 3A11 - mouse >gi 50535 emb CAA42981.1 (X60452) cytochrome P-450IIIA [Mus musculus]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2905	LIB3602-118-Q1-K1-A10	6016708	BLASTX	216	5.00E-17	37	(AC009325) putative protein kinase [Arabidopsis thaliana]
2906	LIB3602-078-Q6-K6-H1	5852164	BLASTX	192	2.00E-18	43	(AJ249389) vacuolar ATPase subunit H [Manduca sexta]
2907	LIB3602-105-Q1-K1-G11	1174853	BLASTX	335	5.00E-31	48	UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42) >gi 481811 pir S39483 ubiquitin-conjugating enzyme UBC2-1 - Arabidopsis thaliana >gi 22658 emb CAA48378.1 (X68306) ubiquitin-conjugating enzyme [Arabidop
2908	LIB3602-107-Q1-K1-H4	3478700	BLASTX	236	2.00E-19	39	(AF034387) AFT protein [Arabidopsis thaliana]
2909	LIB3602-061-Q6-K1-B9	2791900	BLASTX	213	8.00E-17	47	(AJ000057) PP7 [Arabidopsis thaliana]
2910	LIB3602-032-Q6-K1-F2	1945479	BLASTX	174	2.00E-12	65	(U96178) fructose-bisphosphate aldolase [Onchocerca volvulus]
2911	LIB3602-102-Q1-K1-H2	7513277	BLASTX	550	3.00E-56	63	probable transmembrane protein TMC - human
2912	LIB3602-105-Q1-K1-G4	6137575	BLASTX	185	2.00E-13	47	Chain A, Structure And Characterization Of Ectothiorhodospira Vacuolata Cytochrome B558, A Prokaryotic Homologue Of Cytochrome B5 >gi 5919159 gb AAD56233.1 (AF183259) cytochrome b558 [Ectothiorhodospira vacuolata]
2913	LIB3602-001-P1-K6-E3	7449902	BLASTX	172	2.00E-12	58	probable 12-oxophytodienoate reductase (EC 1.3.1.42) CPRD8, drought-inducible - cowpea >gi 1854443 dbj BAA12160.1 (D83970) CPRD8 protein [Vigna unguiculata]
2914	LIB3602-025-Q6-K1-E7	7019666	BLASTX	507	3.00E-51	58	(AL132954) putative protein [Arabidopsis thaliana]
2915	LIB3602-062-Q6-K1-G9	7485705	BLASTX	421	4.00E-41	50	hypothetical protein F18B3.240 - Arabidopsis thaliana >gi 4835247 emb CAB42925.1 (AL049862) putative tRNA synthetase [Arabidopsis thaliana]
2916	LIB3602-047-Q6-K1-G10	7486272	BLASTX	532	3.00E-54	62	hypothetical protein F28A21.220 - Arabidopsis thaliana >gi 4539400 emb CAB37466.1 (AL035526) putative protein [Arabidopsis thaliana] >gi 7268675 emb CAB78883.1 (AL161549) putative protein [Arabidopsis thaliana]
2917	LIB3602-018-Q6-K1-B10	7486436	BLASTX	174	3.00E-12	28	hypothetical protein F4I1.34 - Arabidopsis thaliana
2918	LIB3602-058-Q6-K1-H8	6630456	BLASTX	298	8.00E-27	45	(AC007190) F23N19.15 [Arabidopsis thaliana]
2919	LIB3602-064-Q1-K6-D1	730456	BLASTX	218	2.00E-17	35	40S RIBOSOMAL PROTEIN S19
2920	LIB3602-049-Q6-K1-G3	7259797	BLASTX	152	1.00E-09	29	(AF216743) epsilon tubulin [Trypanosoma brucei]
2921	LIB3602-090-Q6-K6-C2	683699	BLASTX	151	2.00E-09	58	(Z48229) orf2 [Saccharomyces cerevisiae]
2922	LIB3602-015-Q6-K1-B7	5453603	BLASTX	735	6.00E-78	70	chaperonin containing TCP1, subunit 2 (beta) >gi 6094436 sp P78371 TCPB_HUMAN T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) >gi 2559012 gb AAC96012.1 (AF026293) chaperonin containing t-complex polypeptide 1, beta subunit; CCT-beta [Homo sapie
2923	LIB3602-015-Q6-K1-B3	4105639	BLASTX	367	8.00E-35	74	(AF049356) phytoene desaturase precursor [Oryza sativa]
2924	LIB3602-019-Q6-K1-G1	7433407	BLASTX	481	3.00E-48	79	nifU protein homolog T24H24.11 - Arabidopsis thaliana >gi 3377840 gb AAC28213.1 (AF075598) contains similarity to E. coli nitrogen fixation NIFU protein (GB:AE000339) [Arabidopsis thaliana] >gi 7267164 emb CAB77876.1 (AL161499) putative NifU-like metall
2925	LIB3602-043-Q6-K1-C1	140161	BLASTX	172	4.00E-12	36	HYPOTHETICAL 20.1 KD PROTEIN IN MOG-

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							HTGA INTERGENIC REGION (ORF5) >gi 1073400 pir E56688 protein yaaH - Escherichia coli >gi 41756 emb CAA47931.1 (X67700) ORF5 [Escherichia coli] >gi 1786191 gb AAC73121.1 (AE000111) orf, hypothetical protein [Escherich
2926	LIB3602-045-Q6-K1-F1	7491946	BLASTX	165	3.00E-11	41	hypothetical protein SPCC622.19 - fission yeast (Schizosaccharomyces pombe) >gi 4539271 emb CAA21875.2 (AL033127) hypothetical protein [Schizosaccharomyces pombe]
2927	LIB3602-039-Q6-K1-D4	7387549	BLASTX	600	3.00E-62	67	ACETYLGLUTAMATE KINASE (NAG KINASE) (AGK) (N-ACETYL-L-GLUTAMATE 5-PHOSPHOTRANSFERASE) >gi 7434572 pir S77509 acetylglutamate kinase (EC 2.7.2.8) - Synechocystis sp. (strain PCC 6803) >gi 1652434 dbj BAA17356.1 (D90905) N-acetylglutamate kinase [Synechoc
2928	LIB3602-113-Q1-K1-G12	3334201	BLASTX	223	7.00E-18	60	GLYCINE CLEAVAGE SYSTEM H PROTEIN PRECURSOR >gi 7441701 pir T12561 glycine cleavage system protein H precursor - common ice plant >gi 1724106 gb AAB38501.1 (U79768) glycine cleavage system protein H precursor [Mesembryanthemum crystallinum]
2929	LIB3602-011-Q6-K1-B10	4006910	BLASTX	189	6.00E-14	44	(Z99708) putative protein [Arabidopsis thaliana] >gi 7270601 emb CAB80319.1 (AL161589) putative protein [Arabidopsis thaliana]
2930	LIB3602-111-Q1-K1-A11	7433421	BLASTX	254	1.00E-26	62	5-methyltetrahydrofolate--homocysteine S-methyltransferase (EC 2.1.1.13) - rat >gi 3978143 gb AAD05384.1 (AF034214) methionine synthase; MS [Rattus norvegicus]
2931	LIB3602-071-Q1-K1-B6	6525170	BLASTX	515	2.00E-52	63	(AF189278) ASF1 [Drosophila melanogaster] >gi 7293763 gb AAF49131.1 (AE003516) asf1 gene product [Drosophila melanogaster]
2932	LIB3602-023-Q6-K1-G2	4104764	BLASTX	147	5.00E-09	50	(AF039534) salicylate hydroxylase [Pseudomonas stutzeri]
2933	LIB3602-059-Q6-K1-G5	7434315	BLASTX	278	2.00E-24	44	mitogen-activated protein kinase I (EC 2.7.1.-) - parsley >gi 2231034 emb CAA73323.1 (Y12785) MAP kinase I [Petroselinum crispum]
2934	LIB3602-079-Q6-K6-F4	6692729	BLASTX	223	7.00E-18	46	(AC012679) unknown protein [Arabidopsis thaliana]
2935	LIB3602-028-Q6-K1-H7	267147	BLASTX	336	3.00E-31	57	DNA TOPOISOMERASE I >gi 479841 pir S35521 DNA topoisomerase (EC 5.99.1.2) I - fruit fly (Drosophila melanogaster) >gi 158643 gb AAA28951.1 (M74557) topoisomerase I [Drosophila melanogaster] >gi 1772834 gb AAC24158.1 (U80064) DNA topoisomerase I [Drosop
2936	LIB3602-056-Q6-K1-H3	7022048	BLASTX	182	3.00E-13	43	(AK001028) unnamed protein product [Homo sapiens]
2937	LIB3602-103-Q1-K1-E8	7433412	BLASTX	462	5.00E-46	88	nifU protein homolog T10114.50 - Arabidopsis thaliana >gi 2832672 emb CAA16772.1 (AL021712) nifU-like protein [Arabidopsis thaliana] >gi 7269067 emb CAB79177.1 (AL161556) nifU-like protein [Arabidopsis thaliana]
2938	LIB3602-027-Q6-K1-E1	1352458	BLASTX	471	5.00E-47	54	INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD) >gi 2117507 pir JC4999 IMP dehydrogenase (EC 1.1.1.205) - Arabidopsis

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							thaliana >gi 1100063 gb AAB41940.1 (L34684) IMP dehydrogenase [Arabidopsis thaliana] >gi 4835762 gb AAD30229.
2939	LIB3602-095-Q6-K6-A4	7484827	BLASTX	228	2.00E-18	46	brefeldin A-sensitive Golgi protein LDLC homolog F6I7.50 - Arabidopsis thaliana >gi 4678263 emb CAB41124.1 (AL049657) brefeldin A-sensitive Golgi protein-like [Arabidopsis thaliana] >gi 7269335 emb CAB79394.1 (AL161562) brefeldin A-sensitive Golgi prote
2940	LIB3602-057-Q6-K1-E8	7431479	BLASTX	287	4.00E-38	65	methylnalonate-semialdehyde dehydrogenase (acylating) (EC 1.2.1.27) - fruit fly (Drosophila melanogaster) >gi 2653397 emb CAA15632.1 (AL009147) /prediction=(method:""genefinder"", version:""084"", score:""86.60""); /prediction=(method:""genscan"", versio
2941	LIB3602-068-Q1-K1-H5	6175169	BLASTX	150	2.00E-09	42	(AC011437) unknown protein [Arabidopsis thaliana]
2942	LIB3602-056-Q6-K1-D9	5902359	BLASTX	183	2.00E-13	40	(AC009322) Heat-shock protein [Arabidopsis thaliana] >gi 6453873 gb AAF09057.1 AC011717_24 (AC011717) putative heat-shock protein [Arabidopsis thaliana]
2943	LIB3602-071-Q1-K1-H11	7484809	BLASTX	264	1.00E-22	32	ankyrin repeat-containing protein 2 - Arabidopsis thaliana >gi 5830787 emb CAB54873.1 (AL117188) ankyrin repeat-containing protein 2 [Arabidopsis thaliana] >gi 7270496 emb CAB80261.1 (AL161587) ankyrin repeat-containing protein 2 [Arabidopsis thaliana]
2944	LIB3602-004-Q1-K1-D10	4138880	BLASTN	38	1.00E-11	88	Scenedesmus obliquus plastocyanin (Pcy) gene, Pcy-1 allele, complete cds
2945	LIB3602-049-Q6-K1-C1	4138881	BLASTX	309	5.00E-28	46	(AF114235) plastocyanin [Scenedesmus obliquus]
2946	LIB3602-007-Q1-K1-G8	3461884	BLASTX	145	4.00E-09	61	(AB006082) phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis thaliana] >gi 3461886 dbj BAA32529.1 (AB006083) phosphoribosyl-ATP pyrophosphohydrolase [Arabidopsis thaliana]
2947	LIB3602-048-Q6-K1QA-A8	4966344	BLASTX	157	3.00E-10	44	(AC006341) ESTs gb F15498, gb H37515, gb T41906, gb T22448, gb W43356 and gb T20739 come from this gene. [Arabidopsis thaliana]
2948	LIB3602-018-Q6-K1-F3	417540	BLASTX	449	2.00E-44	61	PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) >gi 7431797 pir T06477 probable pyrroline-5-carboxylate reductase (EC 1.5.1.2) - garden pea >gi 20851 emb CAA44646.1 (X62842) pyrroline carboxylate reductase [Pisum sativum] >gi 445614 prf 190936
2949	LIB3602-046-Q6-K1-C5	7635782	BLASTX	280	1.00E-24	51	(AL353819) 2, 5-diketo-D-gluconic acid reductase related protein [Neurospora crassa]
2950	LIB3602-107-Q1-K1-F8	7487148	BLASTX	484	2.00E-48	59	hypothetical protein T18E12.21 - Arabidopsis thaliana >gi 3548818 gb AAC34490.1 (AC005313) unknown protein [Arabidopsis thaliana]
2951	LIB3602-102-Q1-K1-H4	7206593	BLASTX	280	6.00E-34	59	(AC006608) similar to synaptic glycoprotein SC2 [Caenorhabditis elegans]
2952	LIB3602-117-Q1-K1-B12	70640	BLASTX	223	1.00E-18	100	ubiquitin precursor - Trypanosoma cruzi (fragment) >gi 10674 emb CAA30334.1 (X07451) ubiquitin

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2953	LIB3602-120-Q1-K1-G10	1362064	BLASTX	369	6.00E-52	79	fusion protein (78 AA) [Trypanosoma cruzi] GTP-binding protein - garden pea >gi 871514 emb CAA90079.1 (Z49899) small G protein [Pisum sativum]
2954	LIB3602-095-Q6-K6-E12	6094211	BLASTX	248	7.00E-21	73	PROBABLE SMALL NUCLEAR RIBONUCLEOPROTEIN G (SNRNP-G) (SM PROTEIN G) >gi 3738322 gb AAC63663.1 (AC005170) putative small nuclear ribonucleoprotein G [Arabidopsis thaliana]
2955	LIB3602-112-Q1-K1-E10	3122684	BLASTX	368	7.00E-35	61	50S RIBOSOMAL PROTEIN L18 >gi 2446905 dbj BAA22464.1 (AB000111) 50S ribosomal protein L18 [Synechococcus sp.]
2956	LIB3602-028-Q6-K1-B2	4544445	BLASTX	154	6.00E-10	57	(AC006592) putative pyrophosphate--fructose-6-phosphate 1-phosphotransferase [Arabidopsis thaliana]
2957	LIB3602-067-Q1-K1-C1	5803265	BLASTX	227	2.00E-18	48	(AP000399) similar to protein arginine N-methyl transferase 1 (Q63009) [Oryza sativa]
2958	LIB3602-047-Q6-K1-F6	3915072	BLASTX	266	4.00E-23	68	PROBABLE METHIONYL-TRNA SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS) >gi 7504593 pir T22898 hypothetical protein F58B3.5 - Caenorhabditis elegans >gi 3877884 emb CAA97803.1 (Z73427) Similarity to Yeast methionyl-tRNA synthetase (SW:SYMC_YEAST); cDNA EST (U97568) serine/threonine protein kinase [Arabidopsis thaliana]
2959	LIB3602-028-Q6-K1-A3	2109293	BLASTX	322	1.00E-29	58	probable ABC-type transport protein T23J7.100 - Arabidopsis thaliana >gi 4741194 emb CAB41860.1 (AL049746) ABC transporter-like protein [Arabidopsis thaliana]
2960	LIB3602-065-Q1-K6-D3	7488039	BLASTX	325	4.00E-30	55	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (GAPDH) >gi 66006 pir DEKZGR glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - yeast (Zygosaccharomyces rouxii) >gi 218529 dbj BAA00081.1 (D00134) glyceraldehyde-3-phosphate dehydrogenase [Zygosaccharomyce]
2961	LIB3602-080-Q6-K6-F3	120715	BLASTX	341	9.00E-32	72	DFRA PROTEIN >gi 2736191 gb AAB97678.1 (AF025847) DfrA [Myxococcus xanthus]
2962	LIB3602-094-Q6-K6-C6	3913467	BLASTX	158	2.00E-10	57	GTP-BINDING PROTEIN LEPA >gi 7443608 pir S76959 GTP-binding membrane protein lepA - Synechocystis sp. (strain PCC 6803) >gi 1653961 dbj BAA18871.1 (D90917) LepA [Synechocystis sp.]
2963	LIB3602-009-Q6-K1-C3	2494266	BLASTX	513	5.00E-52	68	(AC006341) >F309.11 [Arabidopsis thaliana]
2964	LIB3602-037-Q6-K1-H7	4966352	BLASTX	273	6.00E-24	42	hypothetical protein C02B10.1 - Caenorhabditis elegans >gi 2702376 gb AAB92016.1 (AF038605)
2965	LIB3602-015-Q6-K1-B10	7495172	BLASTX	250	2.00E-21	47	Similar to acyl-CoA dehydrogenase; coded for by C. elegans cDNA yk58h2.3; coded for by C. elegans cDNA yk466c12.3; coded for by C. elegans cDNA yk258d6.3; coded f
2966	LIB3602-007-Q1-K1-E1	7493715	BLASTX	362	4.00E-34	36	WD repeat protein - fission yeast (Schizosaccharomyces pombe) >gi 5701965 emb CAB52157.1 (AL109736) WD repeat protein [Schizosaccharomyces pombe]
2967	LIB3602-023-Q6-K1-D11	474005	BLASTN	37	5.00E-11	89	Rice mRNA, partial homologous to ribosomal

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SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2968	LIB3602-041-Q6-K1-G7	7019653	BLASTX	471	4.00E-47	57	protein S5 gene (AL132954) spliceosomal-like protein [Arabidopsis thaliana] >gi 7019655 emb CAB75756.1 (AL132954) spliceosomal-like protein [Arabidopsis thaliana]
2969	LIB3602-090-Q6-K6-G1	974301	BLASTN	67	6.00E-29	91	Chlamydomonas reinhardtii ribosomal protein L41 (RPL41) mRNA, complete cds
2970	LIB3602-087-Q6-K1-F12	7486098	BLASTX	189	7.00E-14	49	hypothetical protein F24L7.22 - Arabidopsis thaliana >gi 2914709 gb AAC04499.1 (AC003974) hypothetical protein [Arabidopsis thaliana]
2971	LIB3602-078-Q6-K6-H8	849081	BLASTX	565	5.00E-58	63	(U17900) cyclophilin B precursor [Orpinomyces sp. PC-2]
2972	LIB3602-014-Q6-K1-B4	1346031	BLASTX	536	1.00E-54	57	FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL DIPHOSPHATE SYNTHETASE) (KIAA0032) [INCLUDES: DIMETHYLALLYLTRANSFERASE ; GERANYLTRANSTRANSFERASE]
2973	LIB3602-104-Q1-K1-C1	6094228	BLASTX	371	2.00E-35	71	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi 1724102 gb AAB38499.1 (U79766) S-adenosyl-L-homocystein hydrolase; SAH [Mesembryanthemum crystallinum]
2974	LIB3602-058-Q6-K1-F12	5803275	BLASTX	179	7.00E-13	42	(AP000399) EST AU056133(S20320) corresponds to a region of the predicted gene; similar to Caenorhabditis elegans cosmid D1054; hypothetical protein (Z74030) [Oryza sativa]
2975	LIB3602-005-Q1-K1-G11	3834326	BLASTX	147	6.00E-09	53	(AC005679) Similar to gb AF067141 gamma-glutamyl hydrolase from Arabidopsis thaliana. ESTs gb T46595 and gb AI09918 come from this gene
2976	LIB3602-013-Q6-K1-G4	7431450	BLASTX	359	5.00E-34	61	aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) T17F15.130 - Arabidopsis thaliana >gi 4678328 emb CAB41139.1 (AL049658) aldehyde dehydrogenase (NAD+)-like protein [Arabidopsis thaliana]
2977	LIB3602-021-Q6-K1-F7	1172809	BLASTX	355	7.00E-34	72	60S RIBOSOMAL PROTEIN L10 (QM PROTEIN HOMOLOG) >gi 7447294 pir T02068 probable transcription factor QM - maize >gi 468056 gb AAA17419.1 (U06108) QM protein [Zea mays]
2978	LIB3602-052-Q6-K1-H2	3334230	BLASTX	342	5.00E-32	47	D-HYDANTOINASE (DIHYDROPYRIMIDINASE) (DHPASE) >gi 2828803 gb AAC00209.1 (U84197) D-hydantoinase [Pseudomonas putida]
2979	LIB3602-014-Q6-K1-B7	2811057	BLASTX	164	4.00E-11	34	CHITOSANASE PRECURSOR >gi 7474500 pir C69608 chitosanase csn - Bacillus subtilis >gi 1934630 gb AAB80882.1 (U93875) chitosanase precursor [Bacillus subtilis] >gi 2108281 emb CAA63455.1 (X92868) chitosanase precursor [Bacillus subtilis] >gi 2635134 emb
2980	LIB3602-093-Q6-K6-E2	3738312	BLASTX	270	2.00E-23	38	(AC005309) hypothetical protein [Arabidopsis thaliana]
2981	LIB3602-023-Q6-K1-D6	1172835	BLASTX	338	2.00E-31	75	GTP-BINDING NUCLEAR PROTEIN RAN-A1 >gi 496268 gb AAA73563.1 (L16767) GTP-binding protein [Nicotiana tabacum]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
2982	LIB3602-078-Q6-K6-F11	7435073	BLASTX	209	2.00E-16	41	hypothetical protein T26B15.8 - Arabidopsis thaliana >gi 3298540 gb AAC25934.1 (AC004681) putative carboxymethylenebutenolidase [Arabidopsis thaliana]
2983	LIB3602-080-Q6-K6-D6	5902716	BLASTX	174	1.00E-12	47	ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING INHIBITOR HOMOLOG) (DBI) >gi 7497423 pir T30954 hypothetical protein C44E4.6 - Caenorhabditis elegans >gi 2088729 gb AAB54171.1 (AF003140) Similar to acyl-CoA-binding protein; C44E4.6 [Caenorhabd
2984	LIB3602-016-Q6-K1-B5	1084468	BLASTX	147	4.00E-09	33	hydroxymandelonitrile lyase (EC 4.1.2.11) chain A - sorghum (fragment)
2985	LIB3602-010-Q6-K1-A6	6899925	BLASTX	380	2.00E-36	70	(AL138651) P-glycoprotein-like proetin [Arabidopsis thaliana]
2986	LIB3602-032-Q6-K1-F11	7488412	BLASTX	229	1.00E-18	49	ubiquitin-specific proteinase (EC 3.4.-.-) UBP3 - Arabidopsis thaliana >gi 2347098 gb AAB67966.1 (U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi 4490742 emb CAB38904.1 (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]
2987	LIB3602-102-Q1-K1-E12	3482918	BLASTX	305	1.00E-27	71	(AC003970) Similar to ATP-citrate-lyase [Arabidopsis thaliana]
2988	LIB3602-009-Q6-K1-E1	7379550	BLASTX	160	1.00E-10	40	(AL162754) hypothetical protein NMA0833 [Neisseria meningitidis]
2989	LIB3602-003-Q1-K1-A5	7269961	BLASTX	211	5.00E-17	73	(AL161577) signal recognition particle receptor-like protein [Arabidopsis thaliana]
2990	LIB3602-092-Q6-K6-B1	7439981	BLASTX	146	9.00E-14	68	glycine-rich RNA-binding protein GRP1 - wheat >gi 974605 gb AAA75104.1 (U32310) single-stranded nucleic acid binding protein [Triticum aestivum]
2991	LIB3602-026-Q6-K1-G11	480616	BLASTX	689	1.00E-72	80	chlorophyll a/b binding protein - prince's feather >gi 398599 emb CAA52750.1 (X74732) chlorophyll a/b binding protein [Amaranthus hypochondriacus]
2992	LIB3602-092-Q6-K6-G2	7486479	BLASTX	514	6.00E-52	73	hypothetical protein F6E13.19 - Arabidopsis thaliana >gi 3212877 gb AAC23428.1 (AC004005) putative LEA (late embryogenesis abundant) protein [Arabidopsis thaliana]
2993	LIB3602-055-Q6-K1-H10	5902394	BLASTX	220	1.00E-17	33	(AC008148) Putative phosphoglucomutase [Arabidopsis thaliana]
2994	LIB3602-093-Q6-K6-G6	4574242	BLASTX	463	2.00E-48	78	(AF108725) ribosomal protein S16 [Tortula ruralis]
2995	LIB3602-025-Q6-K1-F7	6714424	BLASTX	554	9.00E-57	81	(AC012328) putative ADP-ribosylation factor [Arabidopsis thaliana]
2996	LIB3602-025-Q6-K1-B3	2129619	BLASTX	325	6.00E-30	73	ribosome-associated protein p40 homolog - Arabidopsis thaliana >gi 1345503 emb CAA61547.1 (X89366) 40kD protein [Arabidopsis thaliana] >gi 2102657 emb CAA71407.1 (Y10379) unnamed protein product [Arabidopsis thaliana]
2997	LIB3602-034-Q6-K1-H11	3738327	BLASTX	220	9.00E-18	39	(AC005170) putative serine carboxypeptidase II [Arabidopsis thaliana]
2998	LIB3602-035-Q1-K1-B9	3738328	BLASTX	397	3.00E-38	54	(AC005170) putative serine carboxypeptidase II [Arabidopsis thaliana]
2999	LIB3602-022-Q6-K1-F6	7489162	BLASTX	510	1.00E-51	68	kinesin-related protein tek1 - common tobacco >gi 1491931 gb AAC49393.1 (U52078) kinesin-like protein [Nicotiana tabacum]

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
3000	LIB3602-026-Q6-K1-G7	7488433	BLASTX	245	2.00E-20	42	zinc finger protein homolog T10M13.22 - Arabidopsis thaliana >gi 3377805 gb AAC28178.1 (AF075597) contains similarity to several apoptosis or programmed cell death proteins such as rat apoptosis protein RP-8 (GB:M80601) [Arabidopsis thaliana] >gi 3912928
3001	LIB3602-025-Q6-K1-D9	6554202	BLASTX	150	2.00E-09	43	(AC011661) T23J18.5 [Arabidopsis thaliana]
3002	LIB3602-082-Q6-K6-E9	1170898	BLASTX	376	1.00E-49	77	MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR >gi 629659 pir S44167 malate dehydrogenase (EC 1.1.1.37), mitochondrial - cider tree >gi 473206 emb CAA55383.1 (X78800) mitochondrial malate dehydrogenase [Eucalyptus gunnii]
3003	LIB3602-052-Q6-K1-B6	7190377	BLASTX	270	1.00E-23	38	(AE002301) ADP, ATP carrier protein [Chlamydia muridarum]
3004	LIB3602-062-Q6-K1-C1	7297593	BLASTX	147	4.00E-09	32	(AE003627) CG4747 gene product [Drosophila melanogaster]
3005	LIB3602-119-Q1-K1-E11	7439992	BLASTX	168	6.00E-12	50	splicing factor RSZp22 - Arabidopsis thaliana >gi 3281869 emb CAA19765.1 (AL031004) RSZp22 splicing factor [Arabidopsis thaliana] >gi 3435094 gb AAD12769.1 (AF033586) 9G8-like SR protein [Arabidopsis thaliana] >gi 7270061 emb CAB79876.1 (AL161579) RSZp
3006	LIB3602-042-Q6-K1-H2	7470311	BLASTX	200	2.00E-15	49	hypothetical protein slr0919 - Synechocystis sp. (strain PCC 6803) >gi 1001227 dbj BAA10467.1 (D64003) hypothetical protein [Synechocystis sp.]
3007	LIB3602-054-Q6-K1-C8	3334244	BLASTX	378	3.00E-36	65	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE) >gi 2113825 emb CAA73691.1 (Y13239) Glyoxalase I [Brassica juncea]
3008	LIB3602-086-Q6-K1-D9	6899939	BLASTX	269	1.00E-23	81	(AL138651) ADP-ribosylation factor-like protein [Arabidopsis thaliana]
3009	LIB3602-092-Q6-K6-B5	498741	BLASTN	325	0	93	H.vulgare (pMaW25) mRNA for beta-ketoacyl-ACP synthase
3010	LIB3602-048-Q6-K1QA-E10	7430935	BLASTX	566	3.00E-58	63	probable cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) - tomato
3011	LIB3602-120-Q1-K1-E6	567890	BLASTX	187	1.00E-13	46	(L37352) beta-galactosidase-complementation protein [unidentified cloning vector]
3012	LIB3602-013-Q6-K1-B3	228698	BLASTX	584	3.00E-60	58	CF1 ATP synthase:SUBUNIT=gamma [Chlamydomonas reinhardtii]
3013	LIB3602-107-Q1-K1-F10	1711381	BLASTX	295	2.00E-26	65	PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT) >gi 7434195 pir T09156 phosphoserine aminotransferase - spinach >gi 1256204 dbj BAA12206.1 (D84061) phosphoserine aminotransferase [Spinacia oleracea]
3014	LIB3602-119-Q1-K1-E9	585876	BLASTX	197	2.00E-15	63	60S RIBOSOMAL PROTEIN L23A (L25) >gi 1084424 pir S48026 ribosomal protein L23a, cytosolic - common tobacco >gi 310935 gb AAA53296.1 (L18908) 60S ribosomal protein L25 [Nicotiana tabacum]
3015	LIB3602-023-Q6-K1-A1	1351905	BLASTX	203	1.00E-15	46	BIFUNCTIONAL ASPARTOKINASE/HOMOSERINE DEHYDROGENASE 2, CHLOROPLAST

Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
							<p>PRECURSOR (AK-HD 2) (AK-HSDH 2) [INCLUDES: ASPARTOKINASE ; HOMOSERINE DEHYDROGENASE] >gi 7434567 pir T02954 aspartate kinase (EC 2.7.2.4) / homoserine dehydrogenase (EC 1.1.1.3) precursor (AF095937) succinate dehydrogenase Ip subunit [Gallus gallus] hypothetical protein T9E8.170 - Arabidopsis thaliana >gi 4584548 emb CAB40778.1 (AL049608) putative protein [Arabidopsis thaliana] >gi 7268046 emb CAB78385.1 (AL161536) putative protein [Arabidopsis thaliana] phosphoglucomutase precursor, chloroplast - spinach >gi 534982 emb CAA53507.1 (X75898) phosphoglucomutase [Spinacia oleracea] (AC007290) putative phosphoprotein phosphatase [Arabidopsis thaliana] NADH-UBIQUINONE OXIDOREDUCTASE B8 SUBUNIT (COMPLEX I-B8) (CI-B8) >gi 346540 pir S28249 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B8 - bovine >gi 246 emb CAA44904.1 (X63219) NADH dehydrogenase [Bos taurus] (AL138647) putative protein [Arabidopsis thaliana] (AU066528) 40S ribosomal protein S9 [Chlamydomonas sp.] Hordeum vulgare (clone ABC167) STS mRNA EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT (EIF-2-BETA) >gi 7522212 pir T17104 translation initiation factor eIF-2 beta chain - apple tree (fragment) >gi 1732361 gb AAC06384.1 (U80269) translation initiation factor 2 beta [Malus domestica] probable prohibitin antiproliferative protein - fission yeast (Schizosaccharomyces pombe) >gi 4176556 emb CAA22869.1 (AL035259) putative prohibitin [Schizosaccharomyces pombe] (AL163003) putative fatty acid synthase [Streptomyces coelicolor A3(2)] PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE (PHS) (4-ALPHA-HYDROXY-TETRAHYDROPTERIN DEHYDRATASE) (PHENYLALANINE HYDROXYLASE-STIMULATING PROTEIN) (PCD) >gi 476742 gb AAA25937.1 (M88627) phenylalanine hydroxylase [Pseudomonas aeruginosa] (AC020579) putative phosphoribosylformylglycinamide synthase [Arabidopsis thaliana] hypothetical protein T19L18.24 - Arabidopsis thaliana >gi 3413717 gb AAC31240.1 (AC004747) unknown protein [Arabidopsis thaliana] glycine-rich RNA-binding protein, low-temperature-responsive - barley >gi 1229138 gb AAB07749.1 (U49482) low</p>
3016	LIB3602-038-Q6-K1-C6	3851612	BLASTX	616	4.00E-64	67	
3017	LIB3602-111-Q1-K1-D4	7450363	BLASTX	477	5.00E-48	76	
3018	LIB3602-017-Q6-K1-G8	7484678	BLASTX	524	3.00E-53	59	
3019	LIB3602-118-Q1-K1-G5	4646217	BLASTX	778	5.00E-83	76	
3020	LIB3602-037-Q6-K1-F2	400515	BLASTX	225	3.00E-18	54	
3021	LIB3602-048-Q6-K1QA-B8	7019681	BLASTX	573	5.00E-59	75	
3022	LIB3602-076-Q6-K6-G9	6440857	BLASTX	678	3.00E-71	77	
3023	LIB3602-092-Q6-K6-H7	904068	BLASTN	66	3.00E-28	92	
3024	LIB3602-051-Q6-K1-G1	2494299	BLASTX	411	3.00E-40	68	
3025	LIB3602-017-Q6-K1-D11	7492850	BLASTX	163	5.00E-11	62	
3026	LIB3602-049-Q6-K1-F5	7414558	BLASTX	265	5.00E-23	55	
3027	LIB3602-004-Q1-K1-B2	1172494	BLASTX	150	3.00E-09	50	
3028	LIB3602-003-Q1-K1-E2	6939228	BLASTX	452	6.00E-45	61	
3029	LIB3602-028-Q6-K1-D4	7487199	BLASTX	265	7.00E-23	42	
3030	LIB3602-113-Q1-K1-B1	7439979	BLASTX	371	2.00E-35	97	

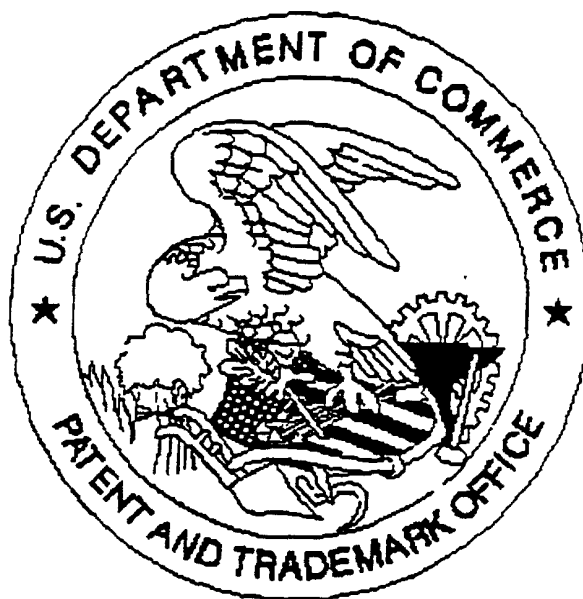
Table 1

SEQ ID No.	Clone ID	NCBI gi	Method	BLAST Score	E value	% Ident	NCBI gi Description
3031	LIB3602-080-Q6-K6-A7	4502327	BLASTX	453	7.00E-45	49	temperature-responsive RNA-binding protein [Hordeum vulgare] AU RNA-binding protein/enoyl-Coenzyme A hydratase precursor >gi 2135070 pir I37195 AU-specific RNA-binding protein / enoyl-CoA hydratase (EC 4.2.1.17) homolog - human >gi 780241 emb CAA56260.1 (X79888) AU-binding protein/Enoyl-CoA hydratase [Homo sapien (AL132957) fructose-bisphosphatase precursor [Arabidopsis thaliana] (AB003712) elongation factor-1alpha [Ampharetidae sp.] (AC006081) unknown protein [Arabidopsis thaliana] hypothetical protein T22J18.13 - Arabidopsis thaliana >gi 3287688 gb AAC25516.1 (AC003979) Contains similarity to ycf37 gene product gb 1001425 from Synechocystis sp. genome gb D63999. ESTs gb T43026, gb R64902, gb Z18169 and gb N37374 come from this ge (AC011664) putative mitochondrial processing peptidase [Arabidopsis thaliana] hypothetical protein F47C12.1 - Caenorhabditis elegans >gi 1397258 gb AAC24388.1 (U61946) contains multiple regions of similarity to EGF-type repeats (PS:PS00022) and sushi (SCR) repeats [Caenorhabditis elegans] (AL138647) putative protein [Arabidopsis thaliana] RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED PROTEIN) >gi 1155265 gb AAA85273.1 (U40219) possible apospory-associated protein [Pennisetum ciliare] (AC018907) unknown protein [Arabidopsis thaliana] (Y14044) geranylgeranyl reductase [Arabidopsis thaliana] (AL138647) putative protein [Arabidopsis thaliana] (AC018907) hypothetical protein [Arabidopsis thaliana]
3032	LIB3602-102-Q1-K1-E6	6822051	BLASTX	328	9.00E-46	64	
3033	LIB3602-083-Q6-K6-C2	3063365	BLASTX	452	1.00E-44	49	
3034	LIB3602-111-Q1-K1-G12	4580461	BLASTX	343	4.00E-32	44	
3035	LIB3602-039-Q6-K1-C5	7487355	BLASTX	186	1.00E-13	57	
3036	LIB3602-060-Q6-K1-C3	6513923	BLASTX	490	3.00E-49	67	
3037	LIB3602-091-Q6-K6-A1	7503664	BLASTX	168	2.00E-11	32	
3038	LIB3602-077-Q6-K6-F4	7019692	BLASTX	479	7.00E-48	61	
3039	LIB3602-004-Q1-K1-E6	3914557	BLASTX	231	4.00E-36	76	
3040	LIB3602-004-Q1-K1-D8	6862923	BLASTX	258	6.00E-22	56	
3041	LIB3602-009-Q6-K1-F6	2828267	BLASTX	262	3.00E-23	75	
3042	LIB3602-102-Q1-K1-A1	7019693	BLASTX	304	7.00E-28	64	
3043	LIB3602-016-Q6-K1-H4	6862921	BLASTX	170	9.00E-12	54	

Table 1 Legend

- SEQ ID No.:** Refers to the sequence identification number of nucleic acids listed in the Sequence Listing.
- Clone ID:** Refers to an assigned cDNA clone ID number.
- NCBI gi:** Refers to National Center for Biotechnology Information GenBank Identifier number which is the best match for a given nucleotide sequence.
- Method:** Refers to the method used in the sequence comparison of the designated nucleotide sequence with the designated GenBank sequence.
- BLAST Score:** Refers to the BLAST score that is generated by sequence comparison of the designated nucleotide sequence with the designated GenBank sequence using the method referenced in the "Method" column.
- E value:** The expected number of distinct segment pairs between two sequences with a score above the bit score for BLAST match.
- % ident:** Refers to the percentage of identically matched nucleotides (or residues) that exist along the length of that portion of the sequences which is aligned by the BLAST comparison to generate the statistical scores presented.
- NCBI gi Description:** A description of the database entry referenced in the "NCBI gi" column.

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